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GenCore version 5.1.6
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November 5, 2004, 18:34:11; Search time 55.4461 Seconds (without alignments) 3839.562 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-797-893-2 1878 1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN 370

Title: Perfect score: Sequence:

BLOSUM62 Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched: 1825181

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Q14807 homo sapien	Aap35923 homo sapi	Q991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae		xenobns		xenobna	Ogggdo xenopus lae		035232 mus musculu	Q61512 oryza sativ								-			pomod.	7		plas	gnm 6	enm s	Q8bll1 mus musculu
SUMMAKIES	Œ	KF22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	691860	AAH70549	Q918K0	Q7ZYL5	Q919A8	Q6GPG0	060845	035232	Q6L512	AAT39162	Q8L7B8	Q9LZ88	08SQQ9	Q7RX60	Q7QDS6	Q862B6	Q961H5	Q8N1X8	KL68 DROME	Q86V <u>S</u> 5	Q8N177	Q9H0F3	Q7RM16	Q8BY99	Q8BZ45	Q8BLL1
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	% Query Match	100.0	100.0	85.4	9.59	65.6	64.0	64.0	64.0	63.8	63.5	63.4	50.6	37.5	33.2	33.2	31.7	31.7	31.1	30.8	30.3	30.0	29.8	29.8	29.6	29.4	29.4	29.4	29.4	29.4	29.4	29.4
	S	1878	1878	1604.5	1232	1232	1202.5	1202.5	1201.5	1197.5	1192.5	1191.5	951	704	623.5	623.5	594.5	594.5	584.5	578	568.5	563	559.5	559	555.5	552.5	552.5	552.5	552	551.5	551.5	551.5
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Q91wd7 mus musculu Q7zuw9 brachydanio	Q9fz77 arabidopsis Q7ksk2 drosophila	Aas65150 drosophil	Q7zxx2 xenopus lae			Ogdde9 xenopus lae				Q7qy55 giardia lam
Q91WD7 Q7ZUW9	Q9FZ77 Q7KSK2	AAS65150	072XX2	Q7SYZ3	Q7PGH1	Q6DDE9	O9LZUS	KLP6 SCHPO	Q9VR <u>K</u> 9	Q7QY55
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29.4	29.3	29.5	29.1	29.0	28.9	28.8	28.6	28.5	28.5	28.4
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3.2	9 6 4 6	36	38	39	40	41	42	43	44	45

# ALIGNMENTS

TELL 1  TREZ HUMAN STANDARD; Q14807; O94814; O9BT46; 16-OCT-2001 (Rel. 40, Last seq 05-JUL-2004 (Rel. 44, Last ann Kinesin-like protein 49; (Kinesin-like protein 49; Name=KIP22; Synonyms=KNSL4, KI HOMO SADiens (Human) Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=96174806; PU TOKAI N., FUJIMOCO-N TSUKITA S., INOUE J. "Kid, a novel kineai "Kid, a novel kineai Chromosomes and the EMBO J. 15:457-467(1	[2] SEQUENCE FROM N.A. TISSUB=Lymphocytoblastoma; TISSUB=Lymphocytoblastoma; MEDLINE=99009323; PubMed=9790757; MEDLINE=99009323; PubMed=9790757; Song J., Murakami H., Yang Z.Q., Koga C., Adati N., Murata T., Geltinger C., Saito-Ohara F., Ikeuchi T., Matsumura M., Itakura K., Kanazawa I., Sun K., Yokoyama K.K.; "Human genes for KNSL4 and MAZ are located close to one another on chromosome 16p11.2."; Genomics 52:374-377(1998).		KIChards S., Worley K.U., hale S., Garla A.D., Cay D. C., Cay Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
KKF7.	R R R R R R R R R S C C	R R R R R R R R R R R R R R R R R R R	**************************************	****

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libsbsib.ch).
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V -> A (in Ref. 2).
APASASOKLSPLOKLSSMDPAMLERLLSLDRLLASOGSQ
-> SSSLCLPETOPPTEAKAAWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
DWTVDPORG (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinesin-motor.

Coiled coil (Potential).

ATP (Potential).

Missing (in Ref. 2).

S -> KV (in Ref. 2).

HTWLGSPEQPGVIPRALMDLLQLTREEGAEGRPWA -> TH
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Coiled coil; DNA-binding; Microtubule; Motor protein;
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GO; GO: 0005634; C:nucleus; TAS.
GO; GO: 0003677; F: DNA binding; TAS.
GO; GO: 0007067; P: microtubule motor activity; TAS.
GO; GO: 0007067; P: microsis; TAS.
InterPro; IPR001563; HHH 1.
InterPro; IPR001563; HHH 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HHH; 2.
SMART; SM00278; HHH; 2.
SMART; SM00279; KINESINHEAVY.
mouse cDNA sequences.";
.. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 1.2e-135;
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GO:0000776; C:kinetochore; TAS.
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Matches 370; Conservative
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koulning M., Raphesl J., Moreira D., Kelley T., Labaer J., Lin Y., Phelan M., Farmer A.;

"Cloning of human full/length CDSs in BD Creator(TM) System Donor
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Catarrhini, Hominidae, Homo.
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EMBL; BT007559; AAP36923.1; -
EMBL; BT0077559; AAP36923.1; -
EMBL; BT007759; AAP36923; 
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Last annotation update)
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 18:34:11; Search time 76.7254 Seconds (without alignments) 3839.562 Million cell updates/sec Run on:

US-10-797-893-4 2589 1 MPAAGGSTQQRRREMAAASA......LEAKMLAQKAEEKENHCPTM 512 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt 02:\*
1: uniprot sprot:\*
2: uniprot trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	- 4	Aap35923 homo gapi	Q991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus l	Q918k0 xenopus lae	Q7zyl5 xenopus lae	Q9i9a8 xenopus lae	Q6gpg0 xenopus lae	O60845 homo sapien	O35232 mus musculu	Q61512 oryza sativ	Aat39162 oryza sat	Q961h5 drosophila	Q817b8 arabidopsis		P46867 drosophila		Q8sqq9 encephalito		Q7qds6 anopheles g	Q9fz77 arabidopsis				Q91784 xenopus lae		Aah70854 xenopus l	Q9gyz0 strongyloce
SOMMAKIES	ΙD	KF22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	691860	AAH70549	Q918K0	Q7ZYL5	Q919A8	Q6GPG0	060845	035232	Q6L512	AAT39162	Ф961Н5	Q8L7B8	09LZ88	KL68_DROME	Q86ZB6	600880	Q7RX60	Q7QDS6	Q9FZ77	Q9VRK9	Q7QY55	Q7M624	KF4A XENLA	QGIRMZ	AAH70854	O9GYZ0
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* Ouery	Match	99.5	99.5	83.4	56.5	56.5	55.5	55.5	55.5	55.2	55.0	54.9	36.5	27.2	24.4	24.4	23.8	23.7	23.7	23.6		23.5		23.3	23.1	22.9	22.6	22.4	22.4	22.4	22.4	22.4
	Score	2577	25	2158.5	1463	1463	1438	1438	1437	1428	1423	1422	946	704	633	633	919	614	614	612	611.5	608.5	604	603.5	597.5	593	584.5	580.5	579.5	579.5	•	579
Result	No.	7	0	e	4	ស	9	7	80	6	10	11	12	13	14	15	16	17		19		21		23	24	25	56	27		29	30	.31

Q91zu5 arabidopsis Q8bz45 mus musculu Q8bl11 mus musculu Q91wd7 mus musculu Q6din5 xenopus tro Q6pb2 homo sapien Aah0364 homo sapien Q86cn3 homo sapien Q95cn3 homo sapien Q9by99 mus musculu Q7zuw9 brachydanio Q98ti xenopus lae Q6gr48 xenopus lae Q6gr48 xenopus lae
0912U5 08B245 08B1L1 091 MD7 06DIN5 06DIN5 06FR42 AAH03664 08FTN3 08FTN3 08FTN3 08FY99 07ZUW9 099FI11 06GR4B
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1058 571 880 1231 787 787 1127 1232 562 862 895 699
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## ALIGNMENTS

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APASAGOKLESPLOKLISSMDPAMLERLLISLDRLLASQGSQ
-> SSEICLPETQPPTEAKAWWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
                                                        R GO; GO:0000776; C:kinetochore; TAS.

RG; GO:0005634; C:nucleus; TAS.
RG; GO:0005634; C:nucleus; TAS.
RG; GO:0003777; F:microtubule motor activity; TAS.
RG; GO:0003777; F:microtubule motor activity; TAS.
RG; GO:0007067; P:mitosis; TAS.
RG; GO:0007067; P:mitosis; TAS.
RG; GO:0007067; P:mitosis; TAS.
RG; GO:0007067; P:mitosis; TAS.
RG; RINGENCOSS; KINESIN MOTOR.
RINGEPRO; IPRO10994; RUVA_2_Iike.
RRNTS; RR00378; HhH1; 2.
RRNTS; RR00378; HhH1; 2.
RRNTS; RR00378; HhH1; 2.
RRNTS; RR00319; KINESIN MOTOR DOMAIN1; 1.
RROSITE; PSO067; KINESIN MOTOR DOMAIN1; 1.
RROSITE; RROSIN MOTOR DOMAIN1; 1.
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HHCPTMLR -> RTIVPQCSG (in Ref. 2)
C6COAC96741DD387 CRC64;
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ATP (Potential).
Missing (in Ref. 2).
S -> KV (in Ref. 2).
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Pred. No. 2.1e-159;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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99.5%; Score 2577; D.
Best Local Similarity 100.0%; Pred. No. 2.1.
Matches 510; Conservative 0; Mismatches
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EMBL; AB017335; BAA33063.1; --
EMBL; AB017331; BAA33063.1; JOINED.
EMBL; AB017334; BAA33063.1; JOINED.
EMBL; BC004352; AAH04352.1; --
EMBL; BC028155; AAH28155.1; --
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73262 MW;
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MIM; 603213; -.
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134
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665 AA;
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Gaps

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0; Indels

3 AAGGSTOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS

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62 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 121
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DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
                                                                                                         62 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP35923;
02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%; Score 2577; DB 2; L
100.0%; Pred. No. 2.1e-159;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 AA.
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Homo sapiens (Human)
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GPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLD 187
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TISSUB=Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                          Length 660;
                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                            INCELTE, ILLU, ILL
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC75575.
                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                          83.4%; Score 2158.5; DB 2 84.8%; Pred. No. 3.8e-132;
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                                                                                                                                                                                                                                                                                                                                                                                32; Mismatches
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InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; RuvA_2_like.
                                                                                                                                                                                                                                                                                                                                                     84.8%;
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 84.8%
Matches 431; Conservative
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STRAIN=FVBAN, TISSUE=Amamary tumor. C3;

MEDLINE=2238825; PubMed=1247932;

MEDLINE=2238825; PubMed=1247932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A tlachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A tlachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A particular R.P., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

B trapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Hichard M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Hiting M., Touchman J.W., Green B.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Kraywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                              RSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 302
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                                AARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPAS
                                                                                                                                                                                                                                                                                                                                                                             ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin family member 22.
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GO; GO:0000785; C:chromatin; IDA.
GO; GO:0005819; C:spindle; IDA.
InterPro; IPR003S83; HHH.1.
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HSSP; P33173; 115S.
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarsen M.B., Bonaldo M.E., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garzin A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ahikebley R.W., Touchman J.W., Cheen B.D., Dickson M.C., Sanchez A.B., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Ageneration and initial analysis of more than 15,000 full-length human
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
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larity 60.3%; Pred. No. 7.8e-87;
Conservative 79; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ of the EMBL; BC063996.1;
EMBL; BC063996, AA#61896.1;
InterPro; IPR011752; kinesin motor.
InterPro; IPR010994; RuvA_2_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
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Matches 292; Conserv
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A trausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Attachner R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pottenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Tonaldo M.F., Carainar T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tonaldo M.F., Carainar P.D., Mullahy S.J.,
A Richards S.M., McKernan K.J., Malek J.A., Gunnarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Wilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Mitting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
A Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
A Gones S.J., Marra M.A.,
B. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFDAFYGDSATQREIYMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPSQPGVIP
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                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis, (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC063896; AAH63896.1; -.
Hypothetical protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                             25-MAR-2004 (TrEMBLrel. 27, Created)
25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                         Hypothetical protein MGC75575
MGC75575.
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Matches 292; Conservative
     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8364;
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AAH63896
AAH63896;
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FISSUE=Embryo;
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WEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-228828.L., Felingold E.A., Grouse L.H., Derge J.G.,

MISCHOLL S.F., Zeeberg B., Buschew K.H., Schaefer C.F., Bhat N.K.,

MEDLINE-2. Marusina K., Farmer A.A., Rang J., Haich F.,

MEDLINE-2. Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDLINE-2. Marusina M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MEDLINE-2. Marusina M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MEDLINE-2. Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MILIAON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILIAON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Marting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Marting M., Maran J.W., Green E.D., Dickson M.C.,

Moriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Moriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Moriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Medriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Moriguez M., Marra M.A.;

Mones S.J., Marra M.A.;

Medneration and initial analysis of more than 15,000 full-length human
                                                                                             SEQUENCE FROM N.A.
MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                          388 KLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQK--LSSMDPAMLERLL
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Xkid, a chromokinesin required for chromosome alignment on the
                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Kinesin (Hypothetical protein) (Chromokinesin Xkid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                    651 AA.
                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metaphase plate.";
Cell 102:425-435(2000).
                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
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SEQUENCE FROM N.A.
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                                                                                                                                                     KENH 508
                                                                                                                                                                               KSTN 482
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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149 PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRILLODSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLOPHALGP 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 YOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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                                                                                                                                                                                                        separation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS0061; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 651 AA; 73065 MW; C2ABAS61C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Blaetula;
McGarry T.J., Bernal T., Funabiki H., Kirschner M.W.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ249840; CAB71798.1;
EMBL, BC070549; AAH70549.1;
EMBL, RC70549; AAH70549.1;
EMBL, AF267849; AAF82563.1;
HSSP; P33173; 115S.
   R.;
to the EMBL/GenBank/DDBJ databages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0003677; F:ATP binding; IEA.
GO; GO:000377; F:BNA binding; IEA.
GO; GO:000377; F:mctor activity; IEA.
InterPro; IPR010996; DNApol B.N.like.
InterPro; IPR003583; HHH 1.
InterPro; IPR001752; kinesin_motor.
                                                                                                                TISSUE=Blastula;
MEDLINE=99340303; PubMed=10411507;
Zou H., McGarry T.J., Bernal T., Kirschner M.W.;
"Identification of a vertebrate sister-chromatid
involved in transformation and tumorigenesis.";
Science 285:418-422(1999).
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20419288; PubMed=10966104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00225; Kinesin; 1. –
PRINTS; PR00380; KINESINHEAVY.
SWART; SW00278; HhH1; 2.
SWART; SW00129; KISC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 102:411-424(2000)
Klein S., Strausberg
Submitted (MAY-2004)
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RA Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atlachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bara N.K.,
Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bara N.K.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Carainoi P., Prange C.,
Rapleton M., Soares M.B., McKernan K.J., Marake J.A., Gunarate P.H.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McKenn P.J., McKernan K.J., Marke J.A., Gunarate P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S., Wadan A., Young A., Schevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A., Schwerkenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Butterfield Y.S.,
T., "Generic L. Scherchan J. Schmutz J., Wyers R.M., Butterfield Y.S.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J., Myers R.M., Schein J.E.,
T., "Generic L. Scherchan J. Schmutz J. Schmerch A., Schein J.E.,
T., "Generic L. Scherchan J. Scherchan
                                           377 MKRPREETGHIAGSQKRKKSKNDSTE--SSPN-SSMDTAGKQKLN----LATLDPAVVER 429
                                                                                                                                                                                         LISIDRILLASQGSQGAPILISTPKRERWVIMKTVEEKDIBIERLKTKQKELEAKMLAQKAB 503
387 VKLSQKE---LLGPPEAKRARGPEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLER
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13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Kenopus laevis (African clawed frog).
Eukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Richardson P.;
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60.1%; Pred. No. 3.4e-85;
iive 80; Mismatches 100; Indels 14;
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
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SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
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proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=22388257; PubMed=12477932;
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NCBI_TaxID=8355;
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TISSUE=Embryo;
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Gaps

Best Local Similarity 60.1 Matches 292; Conservative

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The Xenopus chromokinesin Xkid is essential for metaphase chromosome alignment and must be degraded to allow anaphase chromosome alignment and must be degraded to allow anaphase chromosome alignment and must be degraded to allow anaphase chromosome are alignment and must be degraded to allow anaphase chromosome are alignment and must be degraded to allow anaphase chromosome are alignment.";

Cell 102:411-424[2000]

EMBL; APZ67850; AAP82564.1; -.

RESP; P33173; 1158.

GO; GO:0005875; Cintracellular; IEA.

GO; GO:0005875; Cintracellular; IEA.

GO; GO:0003777; F:DNA binding; IEA.

GO; GO:0003777; F:motor activity; IEA.

GO; GO:0003777; F:motor activity; IEA.

GO; GO:0003774; F:motor activity; IEA.

RO; GO:0003774; F:mot
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                              89 YOFDAFYGERSTQODIYAGSYOPILRHLLEGONASVLAYGPTGAGKTHTMLGSPEOPGVI
                                                                                                                                   PRALMDLIQLTREEGA--EGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                          LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-1004 (TrEMBLrel. 26, Last annotation update)
Xenopus laevis (African clawed frog).
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330 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIINKPFSRETTQTVAQPA 389
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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SEQUENCE FROM N.A.
MEDLINE=20419289; PubMed=10966105;
Antonio_C., Ferby I., Wilhelm H., Jones M., Karsenti E.,
                                                                                                                                                                                                                                                      82; Mismatches 106; Indels
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Last annotation update)
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                                                                                                                                                                                                                  Score 1428;
Pred. No. 1.
                                                                                    PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PROSITE; PS50067; KINESIN MOTOR DOMAIN2; ATP-binding; Microtubule; Motor protein.
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                         PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                  59.4%;
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Cell 102:425-435(2000)
                                                                                                                                                                        663 AA;
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SEQUENCE
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                                                                                                                                                                  RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK 88
                                                                                                                                                                                          YOPDAFYGERSTQODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                             14;
                                                                                      Length 651;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC043733; AAH43733.1; -.
R HSSP; P31773; L15S.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:microtubule associated complex; IEA.
R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003777; F:DNA binding; IEA.
GO; GO:0003774; F:MAP binding; IEA.
R HICTPRO; IPR019996; DNApol_B N.like.
R InterPro; IPR001995; Kinēsin_motor.
R InterPro; IPR001752; Kinēsin_motor.
                                                                                55.5%; Score 1437; DB 2; Length 6 60.1%; Pred. No. 4e-85; .ive 80; Mismatches 100; Indels
                         r_protein.
C4EF79801E603C13
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1. ATP-binding; Microtubule; Motor protein. SEQUENCE 651 AA; 73091 MW; C4EF79801E60:
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                                                                                                   al Similarity 60.1% 292; Conservative
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NCBI_TaxID=8355;
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TISSUE=Embryo;
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                                                                                                                                                                                                                         89 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                                                                                                                                                                           PRALMDLLOLTR---EEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                               LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                            267 REGKLYLIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                            8;
                                                                                                                                                                          Length 650;
                                                                                                                                                                          55.0%; Score 1423; DB 2; Length 6
59.4%; Pred. No. 3.2e-84;
ive 81; Mismatches 107; Indels
                                                                                                                              PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor procesin.
SEQUENCE 650 RA; 73027 WW; EA8415BC4B9B0F4A CRC64;
 HSSP, P3373; 1155.

GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:000577; F:DYB binding; IEA.
GO; GO:0003677; F:DNB binding; IEA.
GO; GO:0003677; F:DNB binding; IEA.
InterPro; IPR010996; DNAPOl B.N_like.
InterPro; IPR003583; HHM_1.
InterPro; IPR003583; Kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             631 AA.
                                                                                             pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM0078; Hhll; 2.
SMART; SM00129; KISc; 1.
                                                                                                                                                                                      Best Local Similarity 59.4 Matches 287; Conservative
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NCBI_TaxID=8355;
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05-JUL-2004
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RA Strausberg R.L., Febigold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Febigold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Tobhlywiki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Serwing A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Scheutz J., Myers R.M., Butterfield Y.S.,
RA Kodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Tand mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 ARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO73177; AAH73177.1; -.
InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; RuvA 2_like.
PAGN; PR00325; Kinesin, 1.
PRINTS; PR00325; KINESINHEAVY.
PRINTS; PR00309; KINESINHEAVY.
PROSITE; PS00411; KINESIN MOTOR DOWAIN1; 1.
PROSITE; PS00411; KINESIN MOTOR DOWAIN2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; Indels
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SEQUENCE
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SILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLOPHALGPVKLSQKELLGPPE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAPYGERSTQQDIYAGSVQPILRHLLEGGQNA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 61
                371 SRQRKKSKTDSTESSPNSSMESTGRRKIN----LASLDSAVVERLLKIDKILTEKGKKEA
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99425270; PubMed=10493829; Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S., Bichler B.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q."; estures in 12 Mb of DNA sequence from Genomics 60:295-308(1999).
HSSP; P33173; 1161.
                                                     400 AKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGA
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                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMR-2004 (TrEMBLrel. 26, Last annotation update)
51milar to kineain-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-32BAB-12;
Nordata, Chordata, Craniata, Vertebrata;
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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ATP-binding; Microtubule; Motor protein.
SEQUENCE 198 AA; 21567 MW; 1A7FDA95B5A03B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
GU:CFPro; IGO01752; Kinesin_motor.
Ffam; PF00225; Kinesin; 1.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
36.5%; Score 946; DB 2; I
Best Local Similarity 100.0%; Pred. No. 7.6e-54;
Matches 183; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                198
                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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 340
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148

PRT;

PRELIMINARY;

035232

RESULT 13 035232 ID 03523 AC 03523

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61 SGDLVIREDCRGNILIPGLTQKPITSFSDFEQHFLPASRNRAVGATRLNQRSSRSHAVLL 120
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A Yang Z., Hanlon D.W., Marezalek J.R., Goldstein L.S.;

A Yang Z., Hanlon D.W., Marezalek J.R., Goldstein L.S.;

A Yang Z., Hanlon D.W., Marezalek J.R., Goldstein L.S.;

A Tidentification, partial characterization, and genetic mapping of kinesin-like procein genes in mouse.";

I Genomics 45:123-131(1997).

EMBL, ARC13119; AAC39968.1; -.

R MGD, GO:000785; Kiff27.

GO; GO:000785; C:chromatin; IDA.

GO; GO:000785; C:chromatin; IDA.

GO; GO:0005819; C:spindle; IDA.

RR MGD; WINSINHEAVY.

RR Pfam; PRO0325; Kinesin; I.

RR PROSITE; PSO0411; KINESIN MOTOR DOMAIN1; 1.

RR PROSITE; PSO0411; KINESIN MOTOR DOMAIN2; 1.

ATP-binding; Microtubule; Motor protein.

T NON TER 148 148
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative kinesin-like DNA binding protein.
Name=OJ1281_H05.2;
OYYZA sativa (japonica cultivar-group).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 AA; 16596 MW; 0950C265C3B63EB7 CRC64;
                              Last sequence update)
Last annotation update)
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Pred. No. 3e-38;
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92.6%; Pred. No. Jer.
5; Mismatches
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                                                                                 (Fragment)
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                              01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26, Kinesin motor protein KIF22 Name=Kif22;
01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05;
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Matches 137; Conservative
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EMBL; AC117265; AAT39162.1; -. SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F CRC64;

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207 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 266
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Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chao Y.-T., Chang C.-I., Han S.-Y., Haiao S.-H.,
Haiung J.-N., Hau C.-H., Hang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-P.,
Cherza sativa BAC OJ1281 HOS genomic sequence.",
Submitted (JUN-2004) to The EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   147 VIPRALMDILQLTREEGAEGRPWALSVTMSYLEIYQEKVLDILDPASGDLVIREDCRGNI
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation
031281 H05.2.
07228 Eativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maipolantee; Britiposida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
                                                                                                                                                                                                                      50;
                                                                                                                                                                                   Length 584;
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al Similarity 36.1%; Score 633; Dength 58
al Similarity 36.1%; Pred. No. 8.5e-33;
166; Conservative 89; Mismatches 155; Indels
InterPro; IPR000445; HhH.
InterPro; IPR001752; Kinesin_motor.
Pfam; PF00633; HHH; 1.
Pfam; PF00025; Kinesin; 1.
PRINTS; PR00130; KINESINHEAVY.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR_DOMAIN1; 1.
PROSITE; PS50667; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Mcrotubule; Motor_protein.
SEQUENCE 584 AA; 64124 MW; EF829G3A15F9190F CRC64;
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                                                                                                                                                                    31 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
                                                 Gaps
                    20;
24.4%; Score 633; DB 2; Length 58 36.1%; Pred. No. 8.5e-33; ive 89; Mismatches 155; Indels
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                       Matches 166; Conservative
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RESULT 1
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Q91805 xenopus la
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G61512 oryza satu
Q61512 oryza satu
Q61512 oryza satu
Q81708 arabidopsis
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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AAP35923
Q99LC7
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KL68 DROME
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Maximum Match 100%
Listing first 45 summaries
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AAH63896
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AAH70549
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Q7ZYLS
Q919A8
Q6GPG0
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Gapop 10.0 , Gapext 0.5
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035232
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Q86ZB6
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Q91W	07ZC	09F2	094	072	075	Q7P	06D	07K	AAS	KLP(	V 60	070	Q6PI
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886 2	895 2	703 2	1254 2	997 2	389 2	553 2	650 2	750 2	7	784 1	677 2	642 2	834 2
31.2 886 2	31.2 895 2	31.1 703 2	30.9 1254 2	30.9 997 2	30.9 389 2	30.7 553 2	30.6 650 2	30.5 750 2	750 2	30.3 784 1	30.3 677 2	30.2 642 2	30.2 834 2

## ALIGNMENTS

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TISSUBERE FROM N.A.

TISSUBERIAL, and Lung;

MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MISCARI S.F., Zeeberg B.B., Buecow M.H., Schaefer C.F., Bhata N.K.,

MEDLEID M., Sacres M.B., Moore T., Max S.I., Wang J., Heibat N.K.,

MEDLEID M., Sacres M.B., Bonaldo M.F., Caraninci P., Prange C.,

MEDLEID M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

MEDLEID M.J., McKernan R.J., Malek J.J., Mullahy S.J.,

MILIADO D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Miling M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Makealey M., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miling M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blutterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Melterfield Y.S.N., Krzywinski M.I., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Lymphocytoblastoma;
MEDLINE-99009323; PubMed=9790757;
Song J., Murakami H., Yang Z.Q., Koga C., Adati N., Murata T.,
Song J., Marakami H., Yang Z.Q., Ikeuchi T., Matsumura M., Itakura K.,
Kanazawa I., Sun K., Yokoyama K.K.;
"Human genes for KNSL4 and MAZ are located close to one another on
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96174806; PubMed-8599929;
Tokai N., Fujimoto-Nishiyama A., Toyoshima Y., Yonemura S.,
Tsukita S., Inoue J., Yamamoto T.;
"Kid, a novel Kinesin-like DNA binding protein, is localized to
chromosomes and the mitotic spindle.";
EMBO J. 15:457-467(1996).
                              014807; 094814; Q9BT46; 16-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Kinesin-like protein KTF22 (Kinesin-like DNA-binding protein Kinesin-like protein 4). Name=KXF22; Synonyms=KNSL4, KID; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 16p11.2.";
Genomics 52:374-377(1998).
STANDARD;
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Q8by99 Q8bz45 Q8b111

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**Q86v85** 

sapien

Q8ni77 Q9h0£3

plasmodium

Q7rm16

Q7RM16 Q8BY99 Q8BZ45 Q8BLL1

552.5 552.5 552.5 551.5 551.5 551.5

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NCBI_TaxID=9606;
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V -> A (in Ref. 2).
V PASASOKLSPLÖKLSSMDPAMLERLISLDRLLASÖGSÖ
-> SSSLCLPETQPPTEAKAAWTRPCGAPPQLGPSACLPGE
P (in Ref. 2).
ENHCPTMLR -> RTIVPQCSG (in Ref. 2).
4; C6COAC96741DD387 CRC64;
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ATP (Potential).
Missing (in Ref. 2).
FIRMLGSPROPOYPRALMOLLOLTREEGAEGRPWA -> TH
                                                                                PubMed=11146551; DOI=10.1038/8j.onc.1204002;
Retrandi A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S.,
Germani A., Bruzzoni-Giovanelli H., Fellous A., Gisselbrecht S.,
M. Varin-Blank N., Calvo F.;
"SIAH-1 interacts with alpha-tubulin and degrades the kinesin kid by the proteasone pathway duving mitosis.";
The proteasone pathway duving mitosis and meiosis. Binds to the movements of chromosomes during mitosis and meiosis. Binds to microtubules and to DNN Nuclear.

-I- FUNCTION: Kinesin Mediated by SIAH1 and leading to its subsequent proteasonal degradation (Probable).

-I- SUBCELLULAR LOCATION: Mediation (Probable).

-I- SUMILARITY: Belongs to the kinesin-like protein family.
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PRINTS, PRO0380, KINESINHEAVY.
SWART; SW00129; KINESINHEAVY.
SWART; SW00129; KISC; 1.
PROSITE; PSO067; KINESIN WOTOR DOMAIN; 1.
PROSITE; PSO067; KINESIN WOTOR DOMAIN; 1.
PROSITE; PSO067; KINESIN WOTOR DOMAIN; 1.
Nuclear protein; UDI conjugation.
DOWAIN 40 299 Colled coil (Potential).
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GO; GO:0003677; F:NNA binding; TAS.
GO; GO:0003777; F:microtubule motor activity; TAS.
GO; GO:0007067; P:mitcais; TAS.
InterPro; IPR003583; HHH 1.
InterPro; IPR001552; kinesin motor.
InterPro; IPR010994; RuvA_2_like.
                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL; AB01735; BAA33063.1; --
EMBL; AB01733; BAA33063.1; JOINED.
EMBL; AB01734; BAA33063.1; JOINED.
EMBL; BC004352; AA404352.1; --
EMBL; BC02455; AA428155.1; --
EMBL; BC024155; AA428155.1; --
EMBL; BC02915; AR782.0; --
GENOW; HGNC: 6391; KIF22.
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   cDNA sequences.";
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Matches 345; Conservative
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GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET

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LKYOFDAFYGERSTOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGSPEQPG 121
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                                                                                                                                                        LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                            242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                               122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                   SEQUENCE FROM N.A. Kalnines L., Bisenstein S., Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT007259; AAP35923.1; -.
SEQUENCE 665 AA; 73261 MW; C6C0AC96741DD387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 1.2e-128;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
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200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIEIN S., Strauberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
R Malb. BCG6396; AAH6396.1;
R EMBL; BCG6396; AAH6396.1;
R InterPro; IPR010994; RuvA_2 like.
R InterPro; IPR010994; RuvA_2 like.
R PRINTS; PR00380; KINESINHEAVY.
R RAART; SM0129; KISC; I.
R PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
R PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
W ATP-binding; Hypothetical protein; Microtubule; Motor protein.
O SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ñ
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                                                                                                                                                                                                                                                                                                      302 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                  TRILQDSLGGSAHSILIANIAPERRFYQDTISALNFTARSKEVIN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein MGC75575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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68.6%; Pred. No. 2.8e-87;
tive 53; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
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Best Local Similarity 68.6
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8364;
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                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                             261
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(6693R1

OG693R1

OG693R1

OG-30

DT 05-40

OG 90

DD 105-40

OG 90

DD 105-40

OG 740

OG 7
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X STRAINS=FURDAY, STANDER-Nammary tumor. C3;

X Strausberg R.L., Fealigold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahla S.S., Logdellanno N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wickernan K.J., Malek J.J., Hulyk S.J.,

Brownstein M.J., McKernan K.J., Malek J.J., Hulyk S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahlesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 LKYQFDAFYGEKSTQQEVYVGSVQP1LRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003427; AAH03427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PSSO67; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 660 AA; 73189 WW; AA8B99477BC49B3C CRC64;
                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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19; Mismatches 20;
                                                                               660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:100233; Kif22.
GO; GO:0000785; C:chromatin; IDA.
GO; GO:0005819; C:spindle; IDA.
InterPro; IPR00383; HHH 1.
InterPro; IPR01072; kinesin motor.
InterPro; IPR010994; Ruva 2 like.
Pfan; PR00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                  Created)
                                                                            PRT;
                                                                                                                         (TrEMBLrel. 17, C
(TrEMBLrel. 17, L
(TrEMBLrel. 26, L
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                                                                                                                                                                                                                 Kinesin family member 22.
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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Matches 305; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                        01-JUN-2001
01-MAR-2004
                                                                                                                               01-JUN-2001
                                                                                                                                                                                                                                     Name=Kif22;
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Query Match
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                                                                                                                                64 QFDAFYGDSATQREIXMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPSQPGVIP 123
                                                                                                                                                                                            RALMDLLQLTREE--GAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNIL 182
                                                                                                                                                                                                                   244 TGKLYLIDLAGSEDNRRTGNQGIRLKESGAINSSLFTLSKVVDALNQGLPRIPYRDSKLT 303
                                                                                                       OFDAFYGERSTOQDIYAGSYOPILRHLLEGONASYLAYGPTGAGKTHTMLGSPEQPGVIP 124
                        64
                                                                   63
                                                                                                                                                                                                                                                                               183 IPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFROR
                                                                                                                                                                                                                                                                                                                                                                  EGKLYLI DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                               5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQETLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063896; AAH63896.1; -.
Hypothetical protein.
SEQUENCE 639 AA; 71390 MW; F5664F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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TISSUB-Embryo;

XX TISSUB-Embryo;

XX Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

XI Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Feligold B.A., Grouse L.H., Schamen C.M., Schuler G.D.,

XX Rlausers R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

XX Rlausers R.D., Collins F.S., Mactow X.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Antechniko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A stonstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A stonstein M.J., Widdin T.B., Toshiyuki S., Carninci P., Prange C.,

An S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley N.M., Sodersen E.J., Lu X., Gibbs R.A.,

A Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A lalalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A lalakelley R.W., Touchman J.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Antiting M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Rachyminski M.I., Skalska W.A.,

Radeneration and initial analysis of more than 15,000 full-length human
                                           ij
                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                               QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIP 124
                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11)
SEQUENCE FROM N.A.
MEDILINE-20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                                                                                                                                                                                                                RALMDLLQLTREE - - GAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNIL
                                                                                                                                                                                                                                                                        243 EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                                                                                                                                                                                                                                                                                 183 IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQR
                                                                                 5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQETLKY
                                                                                                         |:| : ::| ||||||||||||::|
RVSILDQHKKPSSARVRVAVRLRPYMEKEDEKAPAACVRGLDSQSLEIVNWRNQLETMOY
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                             53;
; Score 1232; DB 2;
; Pred. No. 2.8e-87;
53; Mismatches 53;
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                            68.68;
                                Best Local Similarity 68.6
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metaphase plate.";
Cell 102:425-435(2000).
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NCBI_TaxID=8355;
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                              Similarity
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MEDINE-Embryo;

XX MEDINE-Embryo;

XX Straubberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Xa Straubberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Xa Straubberg R.L., Felngold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

Xa Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                           137 PRAVRDLLQMSRTAASAPENENWTYTINMSYVEIYQEKVMDLLEPKNKDLPIREDKDHNI 196
                                                                                                                                    LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                               242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL
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Kenopus laevis (African clawed frog),
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.",
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67.8%; Pred. No. 5.7e-85;
ive 52; Mismatches 56; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
Hypothetical protein Protein SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                         317 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIIN
                                                                                                                                                                                                                                                                                                                                                     13-MAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiative.";
Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences.";
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Best Local Similarity 67.8
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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13-MAY-2004
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"Identification of a vertebrate sister-chromatid separation inhibitor involved in transformation and tumorigenesis.";
Science 285:418-422(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
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                                                                     TISSUE=Embryo;
BEDLINE-22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L.; Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein, Microtubule; Motor protein.
SEQUENCE 651 AA; 73065 MW; C2ABA561C4C53C13 CRC64;
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                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases.
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001752; Kineain motor. Pfam; PF00225; Kineain; 1. PRINTS; PR00380; KINESINHEAVY. SMART; SM00278; HHH; 2. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Blastula;
MEDLINE=20419288; PubMed=10966104;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Blastula;
MEDLINE=99340303; PubMed=10411507;
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LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
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                                        PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
YOFDAFYGERSTQODIYAGSYQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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                                                                                       PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLBIANWRNHQETLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20419288; PubMed=10966104; Funabiki H., Murray A.W.; Punabiki H., Murray A.W.; "The Xenopus chromokinesin Xkid is essential for metaphase chromosome alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                        242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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                  LIPGLSOKPISSPADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQRERLAPFRQ
       RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLBIANWRNHQETLK
                                               YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Barrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                            movement.";

call 102:411-424(2000).

RMBL; AR267850; AAF82564.1; -..

RMBL; AR267850; AAF82564.1; -..

RMBL; AR267850; C:intracellular; IEA.

GO; GO:00056275; C:intracellular; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0003577; F:DNA binding; IEA.

GO; GO:0003774; F:motor activity; IEA.

R InterPro; IPR010996; DNApol B.N.like.

R InterPro; IPR001752; Kinesin. notor.

R PRINTS; PR00258; HHH1.1.

R PRINTS; PR002189; KINESINHEAVY.

R SMART; SM00129; KISC; 1...
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 651 AA; 73091 MW; C4EF79801E603C13 CRC64;
                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
11-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Chromokinesin Xkid.
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Matches 23
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90 YQFDAFYGDSASQREIYMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPDQPGVI 149
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RLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLEIANWRNHQETLK
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                            57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO43733; AAH43733.1; -...
HSSP; P33173; 115S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complex; IEA
                                                                                                                                                                                                                                                                                                                   01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment)
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match
Local Similarity 67.5%; Pred. No. 1.4e-84;
les 233; Conservative 52; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0005622; C: intracellular; IEA.
GO; GO: 0005622; C: microtubule associated compl
GO; GO: 0005524; F: ATP binding; IEA.
GO; GO: 000577; F: DNA binding; IEA.
GO; GO: 0003774; F: motor activity; IEA.
InterPro; IPR010996; DNApol_B.N_like.
InterPro; IPR010996; NIAD.
InterPro; IPR01752; Kinesin_motor.
FEam; PF00225; Kinesin; 1.
PRINTS; PR0380; KINESIN; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN; 1.
ATP-binding; Microtubule; Motor protein.
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MEDLINE=22388257; PubMed=12477932;

X. Strausberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

X. Strausberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

X. Altachul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K.,

R. Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Rahas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                316
                                        242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
          182 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PSS0067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
                                                                                                                                                                                                             302 TRLLODSLGGSAHSILJANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073177, AAH73177.1; -.
InterPro; IPR010752; kinsesin motor.
InterPro; IPR010994; RuvA, 2 like.
Pfam; PF00225; Kinesin; 1.
                                                                                                                                                                                                                                             317 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                  631 AA
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917;
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SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                     O6GPG0;
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiative.
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Q6GPG0
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                                  209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQPDAFYGDSASQREIYMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPDQPGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                     TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                330 TRLLQDSLGGSAHSVMITNIAPEQTYYFDTLTALNFAAKSKQIIN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; MGCOtcubule; MOTOR Protein.
SEQUENCE 650 AA; 73027 MW; EA84158C4B9B0F4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.4%; Score 1192.5; DB 3 Best Local Similarity 67.5%; Pred. No. 3.4e-84; Matches 233; Conservative 51; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005624; C:microtubule associated com
GO; GO:0005875; C:microtubule associated
GO; GO:0003674; F:DAP binding; IEA.
GO; GO:000377; F:DAB binding; IEA.
GO; GO:0003774; F:DAB binding; IEA.
InterPro; IPR010996; DABPOL B.N_like.
InterPro; IPR001752; HHH 1.
InterPro; IPR001752; Kineein_motor.
PEam; PF00225; Kineein; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HHH1; 2.
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Cell 102:425-435(2000).
EMBL; AJZ49841; CAB71799.1; -.
HSSP; P33173; 115S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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                                                                                                                             210
                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinesin.
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168 SGDLVIREDCRGNILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLL 227
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                                               108 GKTHTWLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. GKTHTMLGSPEQPGVIPRALMDLLQLARESAEGRPWDVSVAMSYLEIYQEKVLDLLDPA
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name-CA1281 H05.2;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X MEDLINE-9480723; PubMed=9339368;
X MEDLINE-9480722; PubMed=9339368;
A Yang Z., Hanlon D.W., Margzalek J.R., Goldstein L.S.;
A Yang Z., Hanlon D.W., Margzalek J.R., Goldstein L.S.;
A ridentification, partial characterization, and genetic mapping of kineain-11ke protein genes in mouse.";
I Genomics 45:123-131(1997).
R EMBL, AF013119; AAC3968.1; -.
R MGD; MGI-109233; Kif22.
R GO; GO:000785; C:chromatin; IDA.
GO; GO:000785; C:chromatin; IDA.
R GO; GO:0005819; C:spind1e; IDA.
R GO; GO:0005819; C:spind1e; IDA.
R FRINTS; PR00380; KINESIN-MOTOR DOWAIN1; 1.
R PROSITE; PS0041; KINESIN-MOTOR DOWAIN2; 1.
R PROSITE; PS0041; KINESIN-MOTOR DOWAIN2; 1.
R ATP-binding; Microtubule; Motor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.8%; Score 704; DB 2; Length 148; 92.6%; Pred. No. 5.5e-47; tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AA; 16596 MW; 0950C265C3B63EB7 CRC64;
                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin motor protein KIF22 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 92.6
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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SEQUENCE
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M. MEDLINE-99425270; PubMed=10493829;

M. A. Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,

R. A. Pohrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

A. Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S.,

B. Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

R. Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

R. Genomics doilotations and other features in 12 Mb of DNA sequence from the composer of the constant of
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                                                                                                                                                                                                                                                                                                                                              77 ODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTR- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAH
                                                                                                                                                                                                                                                195 ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ARVRVAVRLRPFVDGTAGASDP-PCVRGMDSCSLEIANWRNHOETLKYQFDAFYGERSTQ
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                                                                                                                                      Gaps
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 07, Last sequence update)
Similar to kinesin-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-328A3.2;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                      3,
                                                                     DB 2; Length 631;
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                                                                 67.4%; Score 1191.5; DB 2; Length
69.6%; Pred. No. 3.9e-84;
Live 48; Mismatches 50; Indels
11E8C9AB86EBD3F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.3%; Score 836; DB 2; L
100.0%; Pred. No. 4.2e-57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 AA.
       71084 MW;
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Matches 159; Conservative
                                                                            Query Match
Best Local Similarity 69.69
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-AUG-1998 (TrEMBLrel.
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SEQUENCE FROM N.A.
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Query Match

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SOW KWA WARAN WARA

H. -L.,

us-10-797-893-6.rup

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58 ECYKLDAFFGQESRVCEIFDQEVSAVIPGIPEGTNATVFAYGATGSGKTYTMQGTEDLPG 117
                                                                                                                                                                                                                                                                                                                                                                                               --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
                                                                                                                                                                                                                                                     224 VKGKLNLIDLAGNEDNRRTCNEGIRLQESAKINQSLFALSNVISALNKKEPRIPYRESKL
                                                                                                                                                                                                                               6 LSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDS-CSLEIANWRNHQETLK-
                                                                                                                                                                                                                                                                                                                                                                           122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 OLKGLAWVPVRSLEEFHEIYSIGVQRRKVAHTGLNDVSSRSHAVLSIRITT-----DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
Chen Y.-L., Cheng. C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa BAC OJ1281 H05 genomic sequence.";
Submitted (JUN-2004) to The EMBL, Schwidtabases.
EMBL, AC11285; AAT39162.1;
SEQUENCE, 584 AA; 64124 MW; EF829C3A15F9190F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRILODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                            35.3%; Score 623.5; DB 2; Length 40.9%; Pred. No. 6.4e-40; ive 68; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5, 2004, 18:38:42
                                                                                                                                                            Query Match 35.3
Best Local Similarity 40.9
Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                            Leu H.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATAAATQSQP---VRVVLRVRPHLPSEANSAEAPCVGLLGSHPGGEVTVQLKDQYTSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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0/1281 H05.2.
0ryza Bativa (japonica cultivar-group).
Bukartota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                              Chao Y.-Y. Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Li Y.-F., Lin S.-J., Liu Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-E., Shaw J.-E., Shaw J.-E., Shaw J.-E., Shaw J.-E., InterPro, IPRO10996; DNApol. B. Like.

InterPro, IPRO10996; DNApol. B. Like.

InterPro, IPRO10752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. STRAIN=CV. Nipponbare; Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRILODSLGGNSHAVMIACLNPVE--YQEAVHTVSLAARSRHVTN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PSSO67; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor_protein.
SEQUENCE 584 AA; 64124 MW; EF829C3A15F9190F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       35.3%; Score 623.5; DB 2;
40.9%; Pred. No. 6.4e-40;
tive 68; Mismatches 113;
                                                                                                                                                                                                                                                                              Pfam; PF00633; HHH; 1.
Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
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Matches 141; Conservative
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                                                                   SEQUENCE FROM N.A.
                                    NCBI_TaxID=39947;
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283

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Gaps

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DB 2; Length 584;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2004, 18:34:11; Search time 72.979 Seconds (without alignments) 3839.562 Million cell updates/sec Run on:

US-10-797-893-8 2472 1 MGRCRLSKIGATRRPPPARV......LEAKMLAQKAEEKENHCPTM 487 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		Description	Q14807 homo sapien	Aap35923 homo sapi	Q991c7 mus musculu	Q6p3r1 xenopus tro	Aah63896 xenopus t	Q9i869 xenopus lae	Aah70549 xenopus 1	Q9i8k0 xenopus lae	Q7zyl5 xenopus lae	Q9i9a8 xenopus lae	Q6gpg0 xenopus lae	O60845 homo sapien		Q61512 oryza sativ	യ					Q862b6 botrytis ci			Q7qds6 anopheles g	arabidopsi	Q9vrk9 drosophila	Q7qy55 giardia lam	_	Q91784 xenopus lae	Q6irm2 xenopus lae		Q9gyz0 strongyloce
SUMMARIES		αī	KF22 HUMAN	AAP35923	Q99LC7	Q6P3R1	AAH63896	691860	AAH70549	Q918K0	Q7ZYL5	Q919A8	QGGPG0	060845	035232	Q6L512	AAT39162	Q961H5	Q8L7B8	Q9LZ88	KL68 DROME	Q86ZB6	Q8SQQ9	Q7RX60 .	Q7QDS6	Q9FZ77	Q9VRK9	Q7QY55	Q7M624	KF4A XENLA	Q6 IRM2	AAH70854	05X50
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	Query	Match	99.8	8.66	86.1	59.2	59.5	58.2	58.2	•	57.8	57.6	57.5	33.8	28.5	25.6	25.6	24.9	24.8	24.8	24.8	24.7	24.6	24.4	٠	24.2	•	23.6	23.5	23.4	23.4	23.4	23.4
		Score	2467	2467	2129.5	1463	1463	1438	1438	1437	1428	1423	1422	836	704	633	633	919	614	614	612	611.5	608.5	604	603.5	597.5	593	584.5	580.5	579.5	579.5	•	579
	Result	No.	-	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q8b245 mus musculu Q8b111 mus musculu Q91wd7 mus musculu Q6din5 xenopus tro Q6din5 xenopus tro Q6pkb2 homo sapien Q86tn3 homo sapien Q85239 homo sapien Q8by99 mus musculu Q7zuw9 brachydanio Q98til xenopus lae Q6gx48 xenopus lae Q86xx7 homo sapien Q8bxy7 homo sapien Q8bxy99 mus musculu Q7zuw9 brachydanio Q98til xenopus lae Q66xx7 homo sapien	Q86vs5 homo sapien
QBBZ45 QBBLL1 Q91WD7 Q61WD7 Q6FWB5 Q6FWB3 AAH03664 AAH03664 Q84TN3 KF4A HUMAN QBBY99 Q7ZUW9 Q9BTI1 Q6GR48	Q86VS5
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5777 5777 5777 5775.5 574.5 574.5 574.5 574.5 572 572 573	268
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# ALIGNMENTS

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242
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      Kinesin-motor.
Coiled coil (Potential).
ATP (Potential).
Missing (in Ref. 2).
S -> KV (in Ref. 2).
HTWLGSPEQPGVIPRALMDLLQLTREEGAEGRPWA -> TH
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Coiled coil; DNA-binding; Microtubule; Motor protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENHCPTMLR -> RIIVPQCSG (in Ref. C6C0AC96741DD387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 665;
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99.8%; Score 2467; DB 1; Length 6
Best Local Similarity 100.0%; Pred. No. 4.3e-153;
Matches 486; Conservative 0; Mismatches 0; Indels
      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                  activity; TAS
                                                                                                                                                                                                                                                                                                                                 GO:0005634; C:nucleus; TAS.
GO:0003677; F:nba bindhing; TAS.
GO:000377; F:microtubule motor
GO:0007067; P:mitosis; TAS.
                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003583, HHH 1.
InterPro; IPR001752; kinesin motor.
InterPro; IPR010994; RuvA 2 11ke.
                                                                                                                                                                                                                                               EMBL, AB017335; BAA33063.1; -.
EMBL, AB017333; BAA33063.1; JOINED.
EMBL, AB017334; BAA33063.1; JOINED.
                                                                                                                                                                                                                                                                                                    Genew; HGNC:6391; KIF22.
MIM; 603213; -.
GO; GO:0000776; C:kinetochore; TAS.
                                                                                                                                                                                                                                                                          EMBL; BC004352; AAH04352.1; -. EMBL; BC028155; AAH28155.1; -. HSSP; P33173; 1158.
                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00225; Kinesin; 1—
PRINTS, PR003090; KINESINHEAVY.
SMART; SM0078; HHII; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 E
73262 MW;
                                                                                                                                                                                                                                        EMBL; AB017430; BAA33019.2; -.
mouse cDNA sequences.";
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2 GRCRLSKIGATRRPPPARVRVAVKLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
26 GRCRLSKIGATRRPPPARVRVAVKLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
27 GRCRLSKIGATRRPPPARVRVAVKLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET

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LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLLQDSLGGSAHS111ANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                                                                                                                                                                                                                                              VKLISQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                               386 VKISQKELIGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                        122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Kalfs A., Halleck A., Hines L., Eisenstein S., Kalnine N., Chen X., Rolfs A., Hansel J., Moreira D., Kelley T., LaBaer J., Lin Y., Koundinya M., Rarmer A.; Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinesin-like 4.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, BT007259, AAP35923.1; -
SEQUENCE 665 AA; 73261 MW; C6C0AC96741DD387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.8%; Score 2467; DB 2; L 100.0%; Pred. No. 4.3e-153; ive 0; Mismatches 0;
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Matches 486; Conservative
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NHCPTM 511
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al Similarity 86.3 422; Conservative
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                                                                                                                LI PGLSQKPI SSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
       REGKLYLI DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                  TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                           TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                             VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                      LDRLLASQGSQGAPLLSTPKRERMVLMKTVEBKDLEIERLKTKQKELEAKMLAQKAEEKE
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003427; AAH03427.1;
HSRP; P33173; 115S.
MGD; MGI:109233; Kif22.
MGD; MG:0000785; C:chromatin; IDA.
GO; GO:00005819; C:chromatin; IDA.
InterPro; IPR003583; HHH_1.
                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                   660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences.
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                                                                                                                                    NHCPTM 487
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SEQUENCE FROM N.A.
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01-JUN-2001
                                                                                                                                                                                                                          Name=Kif22;
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LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 LKYQFDAFYGEKSTQQEVYVGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 REGKLYLIDLAGSEDNRRTGNOGIRLKESGAINTSLPVLGKVVDALNOGLPRIPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKLSQKELLGPSEAKKAKGPEESTGSPESTAAPASASQKLSLLQKLSNMDPAMLENLLS
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TISSUB-Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryotar Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                               Length 660;
                                                                                                                                                                                                                                                                                                                            86.1%; Score 2129.5; DB 2; Length
86.3%; Pred. No. 5.5e-131;
ive 29; Mismatches 33; Indels
InterPro; IPR001752; kinesin motor.
InterPro; IRR010994; Ruva_2_like.
Pfam; PP00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; Hhl1; 2.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS0067; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 660 AA; 73189 MW; AA8B99477BC49B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGF3R1,
06-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC75575.
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan R.J., Mallek J.A., Gunaratne P.H.,
RA R., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Raywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
T. Jones S.J., Marra M.A.;
T. and mouse cDNA sequences.",
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PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 639 AA; 71390 MW; FS64F9020A6AlAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 639;
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; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC063986; AAH638991 motor. InterPro; IPR01752; Kinesin motor. InterPro; IPR010994; RuvA_2_like. Pfam; PF00225; Kinesin; 1. PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISS: 1.
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TISSUB-Embryo,

X. Statusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X. Strausberg R.L.,

X. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X. Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

X. Halenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,

X. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,

X. Diatchenko L., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Bronstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Bronstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Anderde S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X. Raha S.S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X. Hilalon D.K., Muzny D.M., Sodergren B.D., Dickson M.C.,

X. Rahakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

X. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

X. Recheration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                                           Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases EMBL, BC061896, AAH63196.1; -. Hypothetical protein. SEQUENCE 619 AA, 71390 MW; F5664F9020A6AlAA CRC64;
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                                                                                 25-MAR-2004 (TrEMBLrel. 27, Created)
25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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2.4e-87;
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                       639
                                                                                                                                                                                           Hypothetical protein MGC75575.
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                              PRELIMINARY;
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WEDLINE=22388257; PubMed=12477932;
WEDLINE=22388257; PubMed=124. Grouse L.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Raheton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R
418
                                                                                                                        421 SLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE-E 479
                                                                                                                                                            478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E., Nebreda A.R.,
                                                                         363 KLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQK--LSSMDPAMLERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Xkid, a chromokinesin required for chromosome alignment on the
                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Kinesin (Hypothetical protein) (Chromokinesin Xkid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                   651 AA.
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MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Cell 102:425-435(2000).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vernos I.;
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Q91869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                             TISSUE=Blastula;
MEDLINE=99340303; PubWed=10411507;
Zou H., McGarry T.J., Bernal T., Kirschner M.W.;
"Identification of a vertebrate sister-chromatid separation inhibitor involved in transformation and tumorigenesis.";
Science 285:418-422(1999).
                                                                                                                                                                                                                           Funabiki H., Murray A.W.;
"The Xenopus chromokinesin Xkid is essential for metaphase chromosome
alignment and must be degraded to allow anaphase chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
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PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Hypothetical protein, Microtubule; Motor protein.
SEQUENCE 651 Aa; 73065 MW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 651;
                                                                                                                                                                                                                                                                                                                                                       58.2%; Score 1438; DB 2; Length 65
60.1%; Pred. No. 1.1e-85;
ive 80; Mismatches 100; Indels
R.\,\it i to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             MEDLINE=20419288; PubMed=10966104;
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SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 292; Conservative
                                                                                                                                                                                                                                                                                             Cell 102:411-424 (2000)
Klein S., Strausberg
Submitted (MAY-2004)
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                                               SEQUENCE FROM N.A.
                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                              TISSUE=Blastula;
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                                                                                                                                                                                                                                                                              movement.";
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                                                                                                                                                                           SEQUENCE
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XX MEDINRE-238825; PubMed=12477932;
XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
XI Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
X Strausberg R.L., Feingold B.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
X Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Hischul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. B., Bonetow R.J., Mang J., Haiteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Brapleton M., Soares M.B., Bonaldo M.F., Carrinci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McZewan P.J., McKernan K.J., Malek J.A., Gunzartne P.H.,
X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
X Halton B.K., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
X Generation and initial analysis of more than 15,000 full-length human
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                                                                    LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAE 478
                                                                                        VKLSQKE---LLGPPEAKRARGPEEEFIGSPBPMAAPASASQKLSPLQKLSSMDPAMLER
                    Gaps
                                                                                                                                                                                                                                                                                      AMH70549;
13-MAY-2004 (TYEMBLRE1. 27, Created)
13-MAY-2004 (TYEMBLRE1. 27, Last sequence update)
13-MAY-2004 (TYEMBLRE1. 27, Last annotation update)
13-MAY-2004 (TYEMBLRE1. 27, Last annotation update)
Hypothetical protein.
Hypothetical devis (African clawed frog).
Eukaryota; Metazca; (Dordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070549; AAH70549.1; -.
Hypothetical protein.
SEQUENCE 651 AA; 73065 WW; C2ABA561C4C53C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                         651 AA
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NCBI_TaxID=8355;
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Best Local Similarity 60.1<sup>1</sup>
Matches 292; Conservative
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                                                                                                                                                -EKENH 483
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                                                                                                                                                                                                                                                                                                                    361
                                                                                124 PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYOEKVLDLLDPASGDLVIREDCRGNI 181
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                TRILIQDSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
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                                                                                                                                                                                                                                                                                                                                                                                  VKLSQKE---LLGPPEAKRARGPEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLER
                                                            64 YOFDAFYGERSTQODIYAGSYOPILRHLLEGONASYLAYGPTGAGKTHTMLGSPEQPGVI
RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=20419288; PubMed=10966104;
MEDLINE=20419288; A.W.; A.W.;
W.The Xenopus chromokinesin Xkid is essential for metaphase (
"The Xenopus chromokinesin Xkid is essential for metaphase (
alignment and must be degraded to allow anaphase chromosome
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(qell 102:411-424(2000).

(gell 102:411-424(2000).

(HSPE) PASTORSO, AAFRESCH.1; -.

(HSPE) PASTORSO, AAFRESCH.1; -.

(GO; GO:0005622; C:intracellular; IEA.

(GO; GO:0005875; C:intracellular; IEA.

(GO; GO:0005774; F:DNA binding; IEA.

(GO; GO:0003774; F:motor activity; IEA.

(InterPro; IPR010996; DNApol.B.N.like.

(InterPro; IPR01095; MHH.1.

(InterPro; IPR01075; Kinesin_motor.

(HEA.) PR025; Kinesin; 1.

(HEA.) PR025; Kinesin; 1.

(HEA.) PR025; Kinesin; 1.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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SMART; SM00129; KISC; 1.
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                                                                                                                                                                                      PRALMDLLQLTREEGA--EGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 LTGKLYLIDLAGSEDNRRTGNQGIRLKESGAINSSLFTLSKVVDALNQGLPRIPYRDSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVREKDLETERLKTKQKELEAKMLAQKAE
                                                                                                                                                               RLSKIGATRRPPPARVRVAVRLRPFVDGTAGA-SDPPCVRGMDSCSLEIANWRNHQETLK
                                                                                                                                                                                                                                             YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
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                                                                                                                         Gaps
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01-JUN 2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin family member 22 (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                         14;
                                                                                      651;
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TISSUB-Embryo:
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC043733; AAH43733.1; -.
HSSP; P33173; 115S.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005824; F:ATP binding; IEA.
GO; GO:0003877; F:DNA binding; IEA.
GO; GO:0003877; F:DNA binding; IEA.
                                                                                  58.1%; Score 1437; DB 2; Length 6 60.1%; Pred. No. 1.3e-85; ive 80; Mismatches 100; Indels
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 651 AA; 73091 MW; C4EF79801E603C13 CRC64;
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GO; GO: 0005825; C:intracellular associated cor
GO; GO: 0005824; F:ATP binding; IEA.
GO; GO: 0003677; F:DNA binding; IEA.
GO; GO: 0003774; F:DNA binding; IEA.
InterPro; IPR010996; DNAPOL.
InterPro; IPR010996; DNAPOL.
InterPro; IPR0109583; HHH 1.
InterPro; IPR001752; kinesin_motor.
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                                                                                                Best Local Similarity 60.18
Matches 292; Conservative
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                                                                                                                                                                                                                                                                                                                                                90 YQFDAFYGDSASQREIYMGSVCHILPHLLIGQNASVFAYGPTGAGKTHTMLGNPDQPGVI
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                                                                                                                                                                                                                                                                                                                                                                                                           64 YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRALMDLLQLTR - - EEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 LIPGVTLKTINSFGDFDEHFIPASQNRTVASTKLNDRSSRSHAVLLIKVQKSQQVAPFRQ
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                            57.8%; Score 1428; DB 2; Length 6
59.4%; Pred. No. 5.1e-85;
ive 82; Mismatches 106; Indels
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MEDLINE=20419289; PubMed=10966105;
Antonio C., Ferby I., Wilhelm H., Jones M., Karsenti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromokinesin required for chromosome alignment
                                                                                                                                                                                    CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                 663 AA; 74538 MW; 3B98B5F3C12C9C22
                                                                                     PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.
PROSITE; PS50067; KINESIN MOTOR_DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
1 1 1
SEQÜENCE 663 AA; 74538 MW; 3B98BSF3C12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog)
Pfam; PF00225; Kinesin; 1.
PRINTS; PR003180; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
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                                                                                                                                                                                                                                                                    Matches 287; Conservative
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metaphase plate.";
Cell 102:425-435(2000)
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NCBL_TaxID=8355;
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initiative.
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                                                                                                                                                                                                                                          64 YOFDAFYGERSTOQDIYAGSYOPILRHLLEGONASYLAYGPTGAGKTHTMLGSPEOPGVI
                                                                                                                                                                                                                                                   Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mypothetical protein.
Nenopus laevis African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TAXID=8355;
                                                                                                                                                                                      8
                                                                                                                                                                      Length 650;
                                                                                                                                                                                       Indels
                                                                                                                           PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS5067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor Protein.
SEQUENCE 650 AA; 73027 MW; EA8415BC4B9B0F4A CRC64;
                            complex; IEA
                                                                                                                                                                    57.6%; Score 1423; DB 2;
59.4%; Pred. No. 1e-84;
trive 81; Mismatches 107;
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                 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005875; C:intracellular; IEA.
GO; GO:0005874; P:ATP binding; IEA.
GO; GO:0003574; P:DNA binding; IEA.
GO; GO:0003774; P:DNA binding; IEA.
InterPro; IPR010996; DNApol_B_Nike.
InterPro; IPR010996; DNApol_B_Nike.
InterPro; IPR001752; kinesin_motor.
                                                                                       Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00278; HhH1; 2.
SMART; SM00129; KISC; 1.
                                                                                                                                                                              Best Local Similarity 59.49
Matches 287; Conservative
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tegneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00411; KINESIN MOTOR DOWAIN1; 1.
PROSITE; PS00471; KINESIN MOTOR DOWAIN2; 1.
ATP-binding; Hypothetical protein; Microtubule; Motor protein.
SEQUENCE 631 AA; 71084 MW; 11E8C9AB8GEBD3F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BEC03177; AAH73177; AAH73177; EMBL; BEC03177; ARM312; Kinesin motor.
InterPro; IPR010994; RuvA_2_like.
Pfam; PF00225; Kinesin, 1.
Pfam; PR00380; KINESINHEAVY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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60.6%; Pred. No. 1.2e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Mismatches
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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Pfam; PF00633; HHH; 1.
Pfam; PF00225; Kinesin; 1.
                            musculus (Mouse).
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                                                                                           NCBI_TaxID=10090;
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Q6L512
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SILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKELLGPPE 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S.,
Eichler E.E., Marris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
Genomics 60:295-308(1999).
EMBL; AC002301; AAC08709.1; -.
                         371 SRQRKKSKTDSTESSPNSSMESTGKRKIN----LASLDSAVVERLLKLDKILTEKGKKEA
                                                                                    375 AKRARGPEEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLISLDRLLASOGSQGA
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
Similar to kinesin-like DNA binding protein (KID).
Name-A-328A3.2;
Name-A-328A3.2;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO, GO:0005875; C:microtubule associated complex; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IRR001725; kinesin_motor.
Fam; PF00225; Kinesin; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 198 AA; 21567 MW; 1A7FDA95B5A03B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKV 160
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin motor protein KIF22 (Fragment).
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315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 GKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA
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                                                                                                                                                                                   MEDLINE=97480723; PubMed=9339368;
MEDLINE=97480723; PubMed=9339368;
MEDLINE=97480721; PubMed=9339368;
MIGHATIFICATION, PATKIAI CHARACTERIZATION, and GENETIC mapping of kinesin-like protein genes in mouse.";
MIGHATIFICATION, PATSIAI CHARACTERIZATION, and GENETIC mapping of Kinesin-like protein genes in mouse.";
MEMBL; AF013119; AAC39968.1; -.
MEMBL; AF013119; AAC39968.1; -.
MEMBL; AF013119; ARC39968.1; -.
MEMBL; AF013119; ARC3968.1; -.
MEMBL; AF013119; ARC3968.1; -.
MEMBL; AF013119; ARC30088.1; -.
MEMBL; ARC01309; KINESIN MOTOR DOMAIN; 1.
MEMBL; PROSITE; PSO0411; KINESIN MOTOR DOMAIN; 1.
MEMBL; PSO0411; KINESIN MOTOR DOMAIN; 1.
MEMBL; PSO0411; MICHALDHE; MOLOT PROTEIN:
MEMBL; MICHALDHE; MOLOT PROTEIN:
MEMBL; MICHALDHE; MOLOT PROTEIN:
MEMBL; MICHALDHE; MOLOT PROTEIN:
MEMBL; MIC
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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AC117265; AAT39162.1;
InterPro; IPR010996; DNApol_B.N_like.
InterPro; IPR000445; HhH.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 VKVDQRERLAPFRQREGKLYLIDLAGSE 255
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.6
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 RECKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
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EMBL, AC117265, AAT39162.1; PROSCENTINE OF CPC64.
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Best Local Similarity 36.1%; Pred. No. 5.1e-33;
Matches 166; Conservative 89; Mismatches 155; Indels
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                        SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOWAIN1; 1.
PROSITE; PS0067; KINESIN MOTOR DOWAIN2; 1.
ATP-binding; Microtubule; Motor protein.
SEQUENCE 584 AA; 64124 MW; EF82263A15F9190F CRC64;
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Query Match

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US-09-724-224-8

'Sequence 8, Application US/09724224

'Patent No. 6387644

'GENERAL INPORMATION:
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                                                                                                                                                                                                                                                   Sequence 4, Application US/10093317

Patent No. 6765043

GENERAL INFORMATION:

APPLICANT: Bereaud, Christophe

TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/10/093,317

CURRENT PILING DATE: 2002-03-06

PRIOR FILING DATE: 200-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                              LEIERLKTKOKELEAKMLAOKAEEKENHCPIM 512
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LENGTH: 512
TYPE: PRT
ORGANISM: Human
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US-10-093-317-4
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## Sequence 35. Application US/09595684B
| Patent No. 6544766
| GENERAL INPORMATION:
| APPLICANT: Beraud, Christophe
| APPLICANT: Bakowicz, Roman
| APPLICANT: Sakowicz, Roman
| APPLICANT: Waisberg, Eugeni
| APPLICANT: Waisberg, Eugeni
| APPLICANT: Wood, Kenneth
| APPLICANT: Wood, Kenneth
| APPLICANT: Wood, Kenneth
| APPLICANT: Wood, Kenneth
| APPLICANT: Wood, Rometh
| APPLICANT: Wood, Senneth
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Matches 510; Conservative
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US-10-093-317-8
; Sequence 8, Application US/10093317
; Sequence 8, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT PILIGATION NUMBER: 09/724,224
; PRIOR APPLICATION NUMBER: 09/724,224
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 8
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                   methods for
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor proteins and met.)
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
FRICK FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRESEQ for Windows Version 4.0
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100.0%; Pred. No. 4.4e-222;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 486; Conservative
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NHCPTM 487
                                                                                                                                                                   TYPE: PRT
ORGANISM: Human
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US-09-724-224-8
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                                                                                              Query Match 95.3%; Score 2467; DB 4; Length 487; Best Local Similarity 100.0%; Pred. No. 4.4e-222; Matches 486; Conservative 0; Mismatches 0; Indels
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Patent No. 6387644

GENERAL INFORMATION:
TITLE OF INVENTION: No. 6387644el motor prot.
TITLE OF INVENTION: their use
FILE REFERENCE: 1044

CURRENT APPLICATION WUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION WUMBER: 09/597,292

PRIOR FILING DATE: 2000-06-20

WUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Human
US-10-093-317-8
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US-09-724-224-2
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LENGTH: 370
TYPE: PRT
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267 RECKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
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302 FVLGKVVDALNGGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 361
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                                                                                                                                                                                                                                                            ; Sequence 6, Application US/09724224
; Betent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud. Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT PILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR APPLICATION NUMBER: 09/597,292
; RADIOR FILING DATE: 2000-06-10
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO SE
; SEQ ID NO SE
; SEQ ID NO SECOND NO SECOND S
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Sequence No. 6762043

GENERAL INFORMATION:

APPLICANT Beraud, Christophe
TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for TITLE OF INVENTION: their use
FILE REBERBENCE: 1044

CURRENT FILING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: 09/724,224

PRIOR PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 345; Conservative
                                                                                                                                            362 AARSKEVIN 370
                                                                                      363 AARSKEVIN 371
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; ORGANISM: Human
US-09-724-224-6
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US-10-093-317-6
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US-09-724-224-6
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                                                                                                          62 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILHHLLEGQNA 121
                                                                                                                                                                             SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
                                                                                                                                                                                                         EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ 242
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              AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
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; Sequence 2, Application US/10093317
; Patent No. 6762043
; GRNERAL INFORMATION:
    APPLICAMT'S Beraud, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION NUMBER: US/10/093,317
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 370
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Best Local Similarity
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ORGANISM: Human
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US-10-093-317-2
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206 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 265
                                  231 SFRSKLHLVDLAGSERQKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGSFVPYRD 290
                                                                                                                                                                                                 291 SKLTRLLQDSLGGNSHTLMIACVSPADSNLEETLSTLRYADRARKIKNKPIVN--IDPHT 348
                                                                                                                                                                                                                                                                                    349 AELNHLKQ------QVQQLQVLLLQAHGGTLPGSINAEPSEN---LQSLMEKNQSLVEE 398
                                                                                                                                                                                                                                                                                                                                          444 LLSLDRLLASQGSQGAPLLSTPKRERWVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAQK 501
                                                                                                                                                                                                                                                                                                                                                                  VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 P--GVIPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPA--SGDLVIRE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRER 260
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                                                                                          266 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--VPYRD
                                                                                                                                                                         324 SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA
                                                                                                                                                                                                                                                           384 IGPVKLSOKELLGPPEAKRARGPEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLER
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APPLICANT: Beraud, Christophe
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: No. 640684el motor proteins and methods for
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 1016
CURRENT FILING NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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Best Local Similarity
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                     VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
                                                                                                                                                                                                                                                                                                                                                                                                    LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 266
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                                                                                                                                                                                                                                     27 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                         Gaps
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Squence 8, Application US/09592054;
Patent No. 6440684;
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe;
APPLICANT: Beraud, Christophe;
APPLICANT: Sakowicz, Roman;
APPLICANT: Wood, Kenneth;
ITLE OF INVENTION: No. 6440684el motor proteins and methods for ITLE OF INVENTION: No. 6440684el motor proteins and methods for FILE REPERENCE: 1016;
CURRENT APPLICATION NUMBER: US/09/592,054;
CURRENT APPLICATION SONOWINGER: US/09/592,054;
CURRENT APPLICATION NUMBER: US/09/592,054
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100.0%; Pred. No. 2e-156;
ive 0; Mismatches 0
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Matches 345, Conservative
SEQ ID NO 6
LENGTH: 346
TYPE: PRT
ORGANISM: Human
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ORGANISM: Human
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US-10-093-317-6
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SEQ ID NO 8
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                                                                                                                            Query Match
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TYPE: PRT

CRGANISM: Human
US-09-592-054-2
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LENGTH: 1232
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284 VPYRDSKLTRLLQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKPIVNID 343
                                                          379 LQPHALGPVK--LSQKELLGPPEAKRARGPEBEBIGSPEPMAAPASASQKLSP-LQKLSS 435
                                                                                                    436 MDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 493
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APPLICANT: Einer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 522
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                                                                                             344 PQTAELNHLKQQVQQLQVL----LLQAHGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09592054
Patent No. 6440684
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            494 EAKMLAQKAEEKE 506
                                                                                                                                                                                                                                                                                                                                                                      444 DLQKLVETLEDQE 456
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US-09-592-054-4
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APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPRENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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Patent No. 6440684
GENERAL INPORMATION:
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; Sequence 2, Application US/09572191
; Patent No. 6355466
; GENERAL INPORMATION:
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466 DLQKLVETLEDQE 478
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DLOKLVETLEDQE 458
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494 EAKMLAQKAEEKE 506
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Best Local Similarity 32.0°
Matches 158; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                methods for
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APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6379912e1 motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/723,262
FURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/572,191
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
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30.9%; Pred. No. 5.4e-43;
ive 97; Mismatches 192; Indels
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: NO. 6355466el motor proteins and
TITLE OF INVENTION: their use
TILE REPERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6379912
                                                                                                                                                                                                                                                            162; Conservative
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ORGANISM: Human
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Best Local S.
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                                                                                 ; Score 561; DB 3; Length 13
; Pred. No. 5.4e-43;
97; Mismatches 192; Indels
                                                                             21.7%;
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Conservative
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Best Local Similarity
Matches 162; Conserv
TYPE: PRT
ORGANISM: Human
                                        US-09-723-262-2
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Search completed: November 5, 2004, 18:46:45 Job time: 22.0023 secs

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## ALIGNMENTS

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. Human kinesin-like DNA binding protein (KID) (SeqID 4). /note= "Encoded by CA" Location/Qualifiers Ź ADC23340 standard; protein; 512 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. 28-NOV-2000; 2000US-00724224 entry) (CYTO-) CYTOKINETICS INC

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a maxure of the target protein that directly/indirectly produces ADP or phosphate.

Claim 1; SEQ ID NO 4; 26pp; English.

This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor

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domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antinfiammastories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 4) of the invention.
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Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasis; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.

US6762043-B1 13-JUL-2004

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular screening for modulators of motor proteins useful for treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and classases, arthritis, graft rejection, inflammatory bowel disease and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not
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ADQ09240 standard; protein; 665 AA

(first entry) 23-SEP-2004

Human KNSL4 protein SEQ ID NO:425.

thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; 

Homo sapiens.

WO2004055050-A2.

01-JUL-2004.

10-DEC-2003; 2003WO-IB006434.

10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P.

(ENDO-) ENDOCUBE SAS. (CNRS ) CNRS CENT NAT RECH SCI

Roussigne M, Girard J, Amalric F,

Clouaire T;

WPI; 2004-525034/50.

N-PSDB; ADQ09241

Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic acid.

Example 47; SEQ ID NO 425; 612pp; English.

The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP family polypoptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive or THAP/ChemoKine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a call comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family comprising a transcription factor decoy described above; (6) methods of modulating the interaction between a nucleic acid and a THAP-family collypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological coll comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide, (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/Chemokine complex

ta a THAP responsive element or that modulates transcription

c at a THAP responsive element or that modulates the transport of a

c chemokine into the nucleus; (10) methods for reducing the symptoms

c associated with a condition selected from excessive or insufficient

angiogenesis, inflammation, metastasis of acarcerous tissue, excessive

cc insufficient apoptosis, cardiovascular disease and neurodegenerative

diseases; symptoms associated with a condition resulting from the

cc activity of a chemokine or a THAP-family polypeptide in an individual; or

mediated by a THAP-family polypeptide in an individual; (11) a vector

c symptoms associated with transcriptional repression or activation

cc modising a THAP-family polypeptide in an individual; (11) a vector

c comprising a THAP-family polypeptide in an individual; (11) a vector

c comprising the vector described above or that expresses a THAP-family

comprising the vector described above or that expresses a THAP-family

comprising the vector described above or that expresses a THAP-family

comprising the vector described above or that expresses a THAP-family

comprising an nucleic acid comprising a THAP responsive promoter,

craction comprrising a nucleic acid comprising a THAP responsive promoter,

craction has antiangiogenic, antinflammatory, cardiovascular,

cytostatic, neuroprotective and osteopathic activities, and can be used

c as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful

composition has present sequence is used in the exemplification of the

confidence or insufficient apoptosis, cardiovascular disease or neurodegenerative

confidence or insufficient apoptosis, cardiovascular disease or neurodegenerative

confidence or invarion 8888888888888888888888888888888888

Sequence 665 AA;

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                                                                                       2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
                                                                                                                                  63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA
                                                                                                                                                                 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA
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                                                                  3 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
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99.5%; Score 2577; DB 8; L
100.0%; Pred. No. 1.1e-231;
ive 0; Mismatches 0;
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Query Match
Best Local Similarity
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ADC23344 ID ADC RESULT 4

ADC23344 standard; protein; 487

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                                                                                                             human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                 Human kinesin-like DNA binding protein (KID) (SeqID 8)
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100.0%; Pred. No. 1.3e-221;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00597292
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target proteins, methods to identify candidate agents that bind to a target biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                                                                                                             422 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEARMLAQKAEEKE
242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                       TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                302 TRILQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTWESLQPHALGP
                                                                                                                                         387 VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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            proliferation disorders such as cancer, hyperplasias, restenois, cardiac proliferation disorders such as cancer, hyperplasias, restenois, cardiac associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, araft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention.
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 screening for modulators of motor proteins useful for treating cellular
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                                                                                                                                                                                    95.3%; Score 2467; DB 8; Length 487; 100.0%; Pred. No. 1.3e-221; ive 0; Mismatches 0; Indels
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1es 486; Conservative
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (b); (c) hybridizes under stringent conditions to (a) and cc encodes a naturally occurring kinase polypeptide; (d) encodes the cc polypeptide in (a), except that it lacks one or more, but not all, of an complement of comman, a catalytic domain, a C- terminal domain, a colled-coll structure region, a spacer region and a C- terminal domain, a colled-coll structure region, a spacer region and a C- cc terminal tail; or (e) is a acomplement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or curronal-associated diseases, and metabolic disorder: The disorders are cc preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, bain, bacteria, infections and electosis, amyoricrophic lateral sclerosis, ciral infections infections caused by fungi, ocular diseases, migraines, pain, bacteria, infections and disorders, attention disorders, cognition disorders, hypotension, hyperrension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant
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                                                                                                                                                                                                                                                                                                                                                 New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
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Pred. No. 4.1e-217;
); Mismatches 0;
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Best Local Similarity 100.0%; Pr
Matches 479; Conservative 0;
                                                                                                                      31-DEC-2002; 2002WO-US041687
                                                                                                                                                             31-DEC-2001; 2001US-0343169P
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                                                                                                                                                                                                                                                                   Grigoriev IV, Sudarsanam
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SUDARSANAM S.
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                                      WO2003057841-A2
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                               metabolic
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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                              PGVI PRALMDLLQLTREEGAEGRPWXLSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG
                                                                                                                                                                                                                                                                                 302 KLTRILLQDSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHAL
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                                                                                                          ETLKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ
                                                                                                                                                                                                                                                                                                                             RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDS
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                                  GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ
                                                                                                                                                                                 PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinesin-like DNA binding protein (KID) (SeqID 2).
1; Mismatches
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20-JUN-2000; 2000US-00597292.
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   424; Conservative
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                        369
                                                                            422
                                                                                                              429
                                                                                                                                                     481
                                                                                                                                                                                       488
   FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF
                        AARSKEVINRPFTNESLOPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPAS
                                                                                                                                                                      ASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERWVLMKTVEEKDL
                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer antigen protein sequence SEQ ID NO:1228.
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                                                                                                                                                                                                                                                                                     AAB56650 standard; protein; 460 AA.
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ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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(ROSE/) F
                                                                                363
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Human

RESULT 7

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8

Identifying a candidate agent as modulator of function of a target

N-PSDB; ADC23337

Score 2151; DB 3; Length 460; Pred. No. 4.6e-192;

83.1**%**; 95.9**%**;

Query Match Best Local Similarity

Sequence 460 AA;

isolated microtubule motor protein, useful for screening modulators

20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. 28-NOV-2000; 2000US-00724224.

(CYTO-) CYTOKINETICS INC

WPI; 2004-532491/51

New

Beraud C;

06-MAR-2002; 2002US-00093317

13-JUL-2004

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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of traget proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomedulators and antinfilammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGNA
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protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                         Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       72.3%; Score 1873; DB 7; L. 100.0%; Pred. No. 3.5e-166; iive 0; Mismatches 0;
                                                                      Claim 1; SEQ ID NO 2; 26pp; English
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Best Local Similarity 100.
Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Sequence 370 AA;
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The invention traces to numeral mistorubuse muctor processing and the invention traces to numeral mistorubuse motor protein and also relates to a method of screening cativity, a method of testing for ATPase activity of microtubule motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cardiac hypertrophy, immune disorders and inflammation, for treating alsorders as conserving the remaining disorders as sociated with KID and for inhibiting KID and for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune cassociated with KID and for inhibiting kID and for treating autoimmune cassociated with KID and for inhibiting KID and for treating autoimmune cassociated with KID and for inhibiting kID and for treating autoimmune continued as any protein subject to interest the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human microtubule motor proteins and the nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF
                                                                                                                                                                                                                                                                                                                      for treating cellular proliferation disorders such acreening modulat hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2; 26pp; English
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Matches 369; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 370 AA;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of traget proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using method or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
                                                                                                                                                                                                                                             human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346;
                                                                                                                                                                                                                    Human kinesin-like DNA binding protein (KID) (SeqID 6).
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68.1%; Score 1763; DB 7; L

Best Local Similarity 100.0%; Pred. No. 6.4e-156;

Matches 345; Conservative 0; Mismatches 0;
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                                                                                                                  ADC23342 standard; protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2000; 2000US-00724224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CYTO-) CYTOKINETICS INC
                       363 AARSKEVIN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-706919/67.
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                       18-DEC-2003
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                                                                                                                                                     ADC23342;
                                                                                    RESULT 10
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPasse activity, a method of testing for ATPasse activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, methods to identify candidate agents that bind to a target protein, modulators of the target cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA and inflammation for inhibiting KDD. The sequences are used for screening for modulators of motor proteins useful for treating callular screening for modulators of motor proteins useful for treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders
                                                                            266
                                                                                                                                                    REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
                                     181
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                                                                                                                                                                             242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                    LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                 147 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                   327 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 371
                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 6; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human microtubule motor protein #3.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; ADQ60231.
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87 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 146 

GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 86 

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associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                    GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                          GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                       LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                                                                              REGKLYLI DLAGSEDNRRTGNKGLRLKESGAI NTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                  VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
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                                                                                            Length 346;
                                                                                                                                                                                                                                                                                                                                                                                          TRILIQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                              TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 371
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO 40128
                                                                                           68.1%; Score 1763; DB 8; L
100.0%; Pred. No. 6.4e-156;
iive 0; Mismatches 0;
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11-JUL-2000; 2000US-00614150
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genes from Drosophila and
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                                                                                                                Matches 345; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                       Similarity
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                                                                      Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
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                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elucidations for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175, and the encoded proteins (ABB57737-Sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                       83 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RE--RGSGVYVPNLHAINCKSVEDMIKVMQVGNKNRTVGFTNMNEHSSRSHAIFMIKIEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD-TETNTIKVGKLNLIDLAGSERQSKTGASAERLKEASKINLALSSLGNVISALAESSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYASRAKSIQNOPIKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 DPQ-----DAKLKEYQEEIERLKRLIGPQQQQRSEKQVTAKKQRVKRPKKETVTKEMSDS
                                                                                                                                                                                                                                                                                                                            :||| : || || : || || 5
5 SRRPGTGSSQTPNECVQVVVRCRPMSNRERSERSPEVVNVYPNRGV----VELQNVVDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                            140 GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 REDCRGN-ILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 RERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLOPHALGPVKLSQ-----KELLGPPEAKRA------RGPEEEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQG
                                                                                                                                                                                                                                                                                                     37 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQVSTIEQPVEDDSDPE---GAESESDKENEAEVAKSNEELERERVEN-SKLAAKLAELE
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APLLSTPKRERMVLMKTVEEKDLEIER-----LKTKQKELEAKMLAQKAEE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                     Length 784;
                                                                                                                                                                                                                                   Score 616; DB 4; Length 78 Pred. No. 6.1e-48; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 22341.
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                                                                                                                                                                                                                                                                   84;
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                                                                                                                                                                                                                                     23.8%;
33.1%;
                                                                                                                                                                                                                                Query Match 23.8*
Best Local Similarity 33.1*
Matches 176; Conservative
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                                                                                                                                                                                                   Sequence 784 AA;
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LOLTREEGAEGRPWALSVIMSYLEIYQEKVLDLIDPASG-DLVIREDCRGNILIPGLSOK 214
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                                                                                                                                                                                                                                                                                                              is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRVAVRLRPFVDG--TAGASDPPCVRGMD-SCSLEIANWRNHQETLKYQFDAFYGERSTQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQG-LPRVPYRDSKLTRLLQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA 4BBT2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 KLSQKEL-LGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLOKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 ARLRKOLEEGDSLEEEPPSSEEEDTADDELEAPLEIELESSTIOAVEKKPKKKEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP---GVIPRALMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                               Disclosure, SEQ ID NO 22341; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.9%; Score 593; DB 4; Length 677; 33.9%; Pred. No. 6.9e-46; Live 78; Mismatches 190; Indels
                                                                                                                         Myers
                                                                                                                         PWD,
             23-MAR-2001; 2001WO-US009231
                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Best Local Similarity 33.99
Matches 167; Conservative
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                                                                                                                         Adams M,
                                                                                                                                                       WPI; 2001-656860/75.
                                                                                        (PEKE ) PE CORP NY
                                                                                                                                                                      N-PSDB; ABL09286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 677 AA;
                                                                                                                         Venter JC,
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antiparkinsonian; virucide, antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; neurological disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                 cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
                  Š
                  ADK40926 standard; protein; 1237
                                                                              Novel human kinase protein #33.
                                                                                                                                                                                                                                                                                                 31-DEC-2001; 2001US-0343169P.
                                                                                                                                                                                                                                                                              31-DEC-2002; 2002WO-US041687.
                                                                                                                                                                                                                                                                                                                                                  Grigoriev IV, Sudarsanam
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                     GRIGORIEV I V.
                                                                                                                                                                                                                                                                                                                              SUDA/) SUDARSANAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1237 AA;
                                                                                                                                                                                                                                      WO2003057841-A2
                                                                                                                                                                                                                  sapiens.
                                                          06-MAY-2004
                                       ADK40926;
                                                                                                                                                                                                                                                                                                                     (GRIG/)
RESULT 14
         ADK40926
                                     497
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474 GGENLLEKAQTQE 486
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The invention elates to novel isolated, enriched or purified nucleic acid molecule molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and complement of (a); (c) hybridizes under stringent conditions to (a) and coordes a naturally occurring kinase polypeptide; (d) encodes the coorditions to (a) and coordes an atural domain, a coiled-coil structure region, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers. Immune-related diseases or disorders, cardiovascular disease, brain or enuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, brain, viral infections infections caused by fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, anyoricrophic lateral sclerosis, corteria, infections caused by fungi, ocular diseases, metrological disorders, dyskinesias, metabolic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant cried to the corresponds to one of the kinase polypeptides of 13; New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and Gaps 59; Indels Query Match
22.3%; Score 578.5; DB 7;
Best Local Similarity 32.4%; Pred. No. 4.1e-44;
Matches 157; Conservative 97; Mismatches 172; Claim 1; SEQ ID NO 33; 491pp; English.

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IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN 205
                                                                                                                                                                                                                                  SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA 383
                                                                                                                                                                                                                                               ||||||||||||||:||::|| ::|
SKLTRILQDSLGGNSHTLMIACVSPADSNLEETLSTLRYADRARKIKNKPIVN--IDPHT 351
                                                                                                                                                                                                                                                                               384 IGPVKLSQKELIGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER 443
                                                                                                                                                                                                                                                                                                 352 AELINHLKQ------QVQQLQVLLLQAHGGTLPGSINAEPSEN----LQSLMEKNQSLVEE 401
                                                                                                                                                                                                                                                                                                                               501
                                                                                                                                                                                                                                                                                                                                           402 NEKLSRCLSKAAGQTAQML----ERIILTEQVNEKLNAKLEELRQHVACKLDLQKLVET 456
 -----VRGMDSCSLEIANWRNHQETLKYQFDAF 94
                                                                                                      YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQP--GV
                                                         444 LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAQK
                                                                                                                                     ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
                                                                                                                                                                                    QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--VPYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; lung cancer antigen; cytostatic; lung cancer; gene therapy;
vaccine; T-cell; tumour.
                    VRVALRCRPLVPKEISEGCOMCLSFVPGETOVVVGTDK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lung specific tumour antigen L 1447p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD49938 standard; protein; 1232 AA.
VRVAVRLRPFVDGTAGASDPPC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2002; 2002US-00116712.
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N-PSDB; ADD49936.
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                                                                                                                                                                                                                                                                                                                                                                          502 AEEKE 506
                                                                                                                                                                                                                                                                                                                                                                                                457 LEDQE 461
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05-OCT-2001;
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The invention relates to an isolated polynuclectide (a) comprising any of the 666 fully defined nucleotide sequences appearing as ADD49269 ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at least 20 contiguous residues of (a); sequences that hybridise to (a) the following sequences having at least 75 or 90% identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide (b) (comprising; sequences encoded by the new polynucleotide; any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 98% identity to the sequence in (a) or (b)), an expression vector comprising the above polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the above expression vector; an isolated antibody, or its antigen-binding fragment, that specifically binds to the above polypeptide, an oligonucleotide that hybridises to the chinds much much of actions and expression expression expression of the conditions, a finite management conditions. polypeptide, polyuciectide or antigen-presenting cells that express the polymeriating to an antigen-presenting cells that express the polymucleotide, under conditions and for a time sufficient to permit the entimulation and/or expansion of T-cells), an isolated T-cell population comprising T-cells prepared by the method, a composition comprising a first component selected from physiological carriers and immunostimulants, and a second component selected from the above polypeptide, polymucleotide, antibody, fusion protein, T-cell population and antigen-presenting cells that express the above polypeptide, crimulating an immunos in a patient (comprising administering to the patient the above composition) treating lung cancer in a patient (comprising administering to the patient the above composition and at least one antibody cited above and a detection reagent, where the detection reagent comprises a reporter group). The composition and attended are useful in diagnosing, preventing and treating cancer, particularly lung cancer. The present sequence is a lung cancer. tunion protein comprising at least one polypoptide cited above, detecting the presence of a cancer in a patient (comprising: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypoptide, or with the oligonucleotide cited above; detecting in the sample an amount of the polypoptide that binding agent, or an amount of a polymucleotide that binds to the binding agent, or an amount of a polymucleotide that binds to polymucleotide that by bridises to polymucleotide that hybridises to polymucleotide that hybridises to the oligonucleotide, or polymucleotide that hybridises to the oligonucleotide that hybridises to the polymucleotide, or polymucleotide that hybridises to the oligonucleotide, to a predetermined cut. off value and then determining the presence of a cancer in the patient), a method for stimulating and/or expanding T-cells specific for a tumour protein (comprising contacting T-cells with the above

Sequence 1232 AA; 

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225 144 200 DCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRER 260 VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES 378 89 49 SDKNSSFRSKLHLVDLAGSEROKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGGF QPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 145 P--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE DPKEGİKİVGLTEKTVLVALDTVSCLEQGNNSRTVASTAMNSQSSRSHALFTISLEQRKK LAPFROREGKLYLIDIAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--45 VRVAVRLRP-------FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY VRVALRCRPLVPKEISEGCOMCLSFVPG----EPQVVVGTDK-----SP Gaps 75; 22.2%; Score 574.5; DB 7; Length 1232; 32.5%; Pred. No. 9.7e-44; ive 97; Mismatches 161; Indels 75; Best Local Similarity 32.5% Matches 160; Conservative 10 90 20 201 166 261 226 Query Match

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New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer.

Claim 1; SEQ ID NO 670; 250pp; English

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286 VPYRDSKLTRLLQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKPIVNID 345	379 LOPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSP-LQKLSS 435	LLQAHGGTI	436 MDPAMLERLISLDRILASQGSQGAPILSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 493	CLSRGLSEAN	494 EAKMLAQKAEEKE 506	446 DLOKIVETLEDQE 458	
286	379 1	346	436 1	391	494	446	
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Search completed: November 5, 2004, 18:44:39 Job time : 107.087 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5, 2004, 18:34:12 ; Search time 10.7872 Seconds (without alignments) 3300.235 Million cell updates/sec November Run on:

US-10-797-893-2 1878 Title: Perfect score: Sequence:

1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN 370

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	kinesin-like DNA b			F25116.11 protein	kinesin heavy chai	kinesin-related or	probable kinesin-1	kinesin-like prote	F22M8.8 protein -	KLP2 protein - Afr	kinesin homolog F2	probable kinesin-r	kinesin-related pr	probable kinesin-1	kinesin-related pr	kinesin-related pr		kinesin-related or		chromokinesin - ch	kinesin-related pr		kinesin homolog KH	kinesin-related pr	o	microtubule-associ	kinesin heavy chai	kinesin-like prote	prot
SUMMARIES	OI	862328	T48258	A55236	A86319	T18277	T47525	T40594	151617	D86151	T30335	T06733	, H84777	, T02017	B84687	S38982	A48669	A56921	B44259	S64238	A56514	A57107	E84792	A53939	T14156	T48959	A54803	T10164	B48835	T46242
	DB	7		~																	~				~	~	~	0	~	~
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*	Query Match	88.7	31.7	29.6	29.3	29.1	28.6	28.5	28.3	28.3	28.1	28.0	27.9	27.8	27.6	27.4	27.4	27.4	27.3	27.3	27.3	27.3	27.2	27.1	27.1	27.1	27.0	27.0	26.9	26.8
	Score	1665	594.5	555.5	550	547	536.5	536	532	531.5	527.5	525	524	521.5	517.5	514.5	514	514	513.5	513.5	513.5	513	511.5	509.5	509.5	508	507.5	507	504.5	504
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G02157	A55289	T51930	T20621	T51932	T40128	A41919	S58691	T38378	T51360	JC5831	S44868	C48835	JN0114	T15822	837711
-	Н	~	N	~	~	н	-	~	N	~	N	~	Ä	~	7
1056	1150	935	928	929	883	963	742	1085	987	793	843	332	1584	1584	1027
26.7	26.6	26.5	26.4	26.4	26.3	26.1	26.1	26.0	26.0	25.9	25.9	25.7	25.7	25.7	25.7
501	200	498.5	495.5	495	494.5	491	490	488.5	488	485.5	485.5	483	482.5	482.5	482

## ALIGNMENTS

	S62328
	kinesin-like DNA binding protein KID - human
	C;Species: Homo sapiens (man)
	C;Date: 23-Aug-1996 #sequence revision 13-Mar-1997 #text change 16-Aug-2004
	C;Accession: S62328
	R; Tokai, N.; Fujimoto-Nishiyama, A.; Tovoshima, Y.; Yopemura, S.; Tsukita, S.; I
	EMBO J. 15, 457-467, 1996
	A: Title: Kid, a novel kinesin-like DNA binding protein. is localized to chromoso
	A; Reference number: S62328; MUID: 96174806; PMID: 8599929
_	A;Accession: S62328
_	A; Status: preliminary; not compared with conceptual translation
_	A; Molecule type: mRNA
_	A;Residues: 1-665 <tox></tox>
	C;Superfamily: kinesin motor domain homology
	C; Keywords: ATP; nucleotide binding; P-loop
	F;44-374/Domain: kinesin motor domain homology < XMOT>
	F,128-135/Region: nucleotide-binding motif A (P-loop)
	Ouery Match 88.7%; Score 1665; DB 2; Length 665;
	Similarity

Inoue, J omes and

> .. 7 29; Indela 1; Mismatches Matches 339; Conservative

7

Gaps

SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN 120 61 SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGN 120 121 AS-VLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGREWALSVTMSYLEI 179 121 AKVVLAYGPTGAGKT-THAGQPRATWGDPAGSHGPPAAHKGGGCRGPAWGLSVTWSYLEI 179 YQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRL 239 9 9 1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 19 180 ò ď ò a ò g Š g δ g δ 8

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RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, N.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Lii, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M. D.; Yu, G.; Eraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q9FZ77; GB: AE005172; NID: 99795601; PIDN: AAF98419.1; GSPDB: GNK
                              A;Cross-references: FlyBase:rbgiuvorsor.
C; Punction:
C; Punction:
C; Punction:
C; Punction:
C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C; Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
C; Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
F; 1349/Domain: head globular #status predicted KMOT>
F; 106-113/Region: nucleotide-binding motif A (P-loop)
F; 106-113/Region: nucleotide-binding motif ced KMOT>
F; 106-113/Region: nucleotide-binding motif ced KMOI>
F; 106-113/Region: nucleotide-binding motificed KMOI>
F; 112/Binding site: ATP 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KEÇRKVFTYDAAYDASATĞTTLYHEVVFPLVSSVLEGFNGCIFAYGQTĞTĞKTFTMEGVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F25116.11 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK-----YQFDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 RERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 HVPYRDSKITRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYGSRAKSIQN 346
                                                                                                                                                                                                                                                                                                                                                                                                          Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 703;
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38.6%; Pred. No. 5.6e-36;
ive 62; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
29.6%; Score 555.5; DB 1;
Best Local Similarity 39.5%; Pred. No. 2.4e-36;
Matches 140; Conservative 56; Mismatches 127;
                       Cross-references: FlyBase: FBgn0004381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
A; Gene: FlyBase: Klp68D; KLP5
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A,Status: preliminary
A,Molecule type: DNA
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Best Local (
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Nylternate names: kinesin-like protein 5; KLP5
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: $45236 # 81298
R;Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Cell Biol. 127, 1041-1048, 1994
A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible rol
A;Reference number: A55236, MUID:95050960; PMID:7525600
A;Recession: A55236
A;Residues: 1-784 <-PES-
A;Residues: 1-784 <-PES-
A;Crose-references: UNIPROT:P46867; GB:UIS974; NID:G595912; PIDN:AAA69929.1; PID:G565096
A;Residues: 1-784 <-PES-
A;Crose-references: UNIPROT:P46867; GB:UIS974; NID:G595912; PIDN:AAA69929.1; PID:G565096
A;Reference number: A1298; MUID:92020874; PMID:1924306
A;Reference number: A41298; MUID:92020874; PMID:1924306
A;Accession: A1298; MUID:92020874; PMID:1924306
A;Accession: Ann.
                                            N.Alternate names: protein T1E22.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48258
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24489
A;Accession: T48258
A;Status: preliminary
A;Aclaus: preliminary
A;Residues: 1-664 < BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STILSMCEKTRSRAE-----ISYYEVYMDRCWDLLEVKDNEIAVWDDKDGQVHLKGLS 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Nap position: 5
A;Introns: 58/3; 128/2; 184/3; 310/1; 378/3; 480/2; 501/3; 535/1; 607/3; 628/3
A;Note: T1E22.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYG-ERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQPGVIPRAL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 MDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLS
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A;Residues: 'TC',222-337,'VRGQV' <STE>
A;Cross-references: GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 594.5; DB 2; Length 6; Pred. No. 1.4e-39; 69; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLGGTSRALMVACLNPGE--YQESLRTVSLAARSRHISN 401
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9LZ88; EMBL:AL162874
A;Experimental source: cultivar Columbia; BAC clone T1E22
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38.6%;
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A;Map position: 3
A;Introms 56/2, 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; 55
A;Note: F16L2.60
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
                Cyaccession: T47225
RiJordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, Submitted to the Protein Sequence Database, March 2000
A;Reference number: 224468
A;Reference number: 224468
A;Reference number: 224468
A;Residuus: preliminary
A;Molecule type: DNA
A;Residues: 1-1058 cJOR>
A;Experimental source: cultivar Columbia; BAC clone F16L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARIHTPVVI----SCN-----ENRREVAATQSIAGKHIDRHFAFDKVFGPASQQXDLYD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREEGAEGRPWALSVTMSYLEIYQEKVLDLLDP------ASGDLVIREDCRGNILI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ-- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
   20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                             3 SIQQRRGGIVSLSPAQTPRSSDKSARESRSSESNSTNRNDKEKGVNVQVILRCRPLSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQPGVIPRALMDLLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 STQQRRREMAAASAA----AISGAGRCRLSKIGATRRPPPAR---VRVAVRLRPFVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 RGLEEEIVSTANEIYKILEKGSAKRRTAETLLNKQSSRSHSIFSITIHIKENTPEGEEMI
                                                                                                                                                                                                                                                                                                               28.6%; Score 536.5; DB 2; 33.1%; Pred. No. 1.2e-34; iive 77; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AGASDPPCVRGMDSCSLEIANWRNHQETLKYQ----
                                                                                                                                                                                                                                                                                                                                                 Matches 134; Conservative
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-784 <PUR>
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Kinesin heavy chain - slime mold (Dictyostelium discoideum)

Cispeciae Dictyostelium discoideum

Cispeciae Dictyostelium discoideum

Cipate: 15-Oct-1999 #text_change 09-Jul-2004

CiAccession: T18277 #squence_revision 15-Oct-1999 #text_change 09-Jul-2004

CiAccession: T18277 #squence_revision 15-Oct-1995

A;RédHostos, B.L.; MCCaffrey, G.; Vale, R.D.

Bubmitted to the EMBL Data Library, November 1995

A;Reference number: Z18853

A;Reference number: Z18853

A;Accession: T18277

A;Accession: T18277

A;Accession: T18277

A;Accession: T18277

A;Accession: T18277

A;Residues: 1-1254 < DEH>

A;Residues: 1-1254 < DEH>

A;Cross-references: UNIPROT:Q94463; EMBL:U41289; NID:g1526990; PID:g1526991; PIDN:AAB077
                                                                                                                                                 427
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                                                                                                                                                                                                                      -:-----GNQNRTTEPTRCNETSSRSHAILQVIVEYKTRDASMNIISRVGKLS 367
                                                                                                                                                                                                   214 PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR--QRECKLY 271
                                                                                                                                                                                                                                                                       LIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STOODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDL--- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQLTREEGAEGRPWALSVTMSYLEIYOEKVLDLLDPASGDLVIREDCRGNILIPGLSQKP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLG 334
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LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK
                                                                                                                                                                                                                                                                                            YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 PPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEI-ANWRNHQETLKYQFDAFYGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.1%; Score 547; DB 2; Length 12:
36.3%; Pred. No. 2.2e-35;
tive 76; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                               SIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368
                                                                                                                                                                                                                                                                                                                                                                  GSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:::|||:| GNSKTSLIINCSPSNNNEHETITTLQPGTRAKTIKN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.1
Best Local Similarity 36.3
Matches 122; Conservative
                                                                                                                            154
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-----FDAFYGERSTQQDIYA 105

62

Gaps

55;

Indels

Length 1058;

157

287

347

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A;Cross-references: UNIPROT:059751; EMBL:AL023587; PIDN:CAA19043.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; cosmid c649
*Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, July 1998
A;Reference number: 221861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 464-784 <WOO>.
A;Cross-references: EMBL:AL031154; PIDN:CAA20063.1; GSPDB:GN00067; SPDB:SPBC1685.15c
A;Experimental source: strain 972h-; cosmid c1685
C;Genetics:
                                                                                                                                                                                                                                                                                                                                              В.
                                                                                                                                                                                                                                                                        probable kinesin-like protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Decies: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                   TRLLRESLGGKTKTCVIATISPSIHCLEETLSTLDYAHRAKNIKN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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kinesin-related protein-like - Arabidopsis thaliana N;Alternate names: protein F16L2.60 C;Species: Arabidopsis thaliana (mouse-ear cress)

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Rithelogis, A.; Beker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R; Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

Nature 408, 186-820, 2000

Rixer, Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II A; Muthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II A; W. W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MuID:21016719; PMID:11130712

A; Residues: 1-885 < STO>

A; Mesidues: 1-885 < STO>

A; Residues: 1-865 < ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9LPC6; GB:AE005172; NID:g8570446; PIDN:AAF76473.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ę,
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                                                                                                                                          MDLLQLTREEGAEGRP-WALSVINSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI 207
                                                                                                                                                                                                                                                                                                                                        PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQRE 267
                                                                                                                                                                                                                                                                                                                                                                         GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR---VPYRDSK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F22M8.8 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGQNASVLAYGPTGAGKTHTM--LGSPEOP--GVIPRALMDLLQLTREEGAEGRPWALS
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                                                                                                            99 TOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGS-----PEQP--GVIPRAL
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VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETL--
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28.3%; Score 531.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 2.4e-34;
Matches 137; Conservative 72; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                                                                                          -----QETL-----KYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQ 119
                                                                                                                                                                                                                                                                                                                                                                                           NASVLAYGPŢGAGKTHŢMLGSPEOPGVI---PRALMDLLQLTREEGAEGRPWALSVTMSY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEIYNEKIRDLLVQDPLSMEKPKSLNICEDAEQNVSVPGLSYFTPTNLEEVMEIIIRGNS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRIVGATRINQRSSRSHAVILVKVDQRERLAPFRQREGK------LYLIDLAGSED 280
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                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                99
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                                                                                                                              Length 784;
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28.3%; Score 532; DB 2; Length 12
Best Local Similarity 36.1%; Pred. No. 3.4e-34;
Matches 125; Conservative 74; Mismatches 113; Indels
                                                                                                                              Query Match
28.5%; Score 536; DB 2; Length 78
Best Local Similarity 35.5%; Pred. No. 8.7e-35;
Matches 139; Conservative 61; Mismatches 116; Indels
                                                                                                                                                                                                                                             44 VRVAVRLRPFVDGTAG--ASDPPCVRGMDSCSLEIANWRNH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHSILIANIAPERRFYLDTVSALNFAARSKEV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::| |:| :| |:| 389
CRTCMIVCISPSSEHYDETHNTLKYGNRAKNI 389
                        SPDB:SPBC649.01c; SPDB:SPBC1685.15c
                                                         position: 2
                        A,Gene: SPDB:SPB
A,Map position: A,Introns: 11/1
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probable kinesin-related cytokinesis protein (imported) - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress)
("Species: Arabidopsis thaliana (mouse-ear cress)
("Species: O2-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
("Accession: H84777
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
Affile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84777
A;Accession: H84777
A;Accession: Preliminary
A;Accession: DNA
A;Residues: 1-1056 <STO>
A;Cross-references: UNIPROT:PB2266; GB:AE002093; NID:g4510356; PIDN:AAD21445.1; GSPDB:GN
                      A;Map position: 3
A;Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3; C;Superfamily: Kinesin-related protein KLP61F; Kinesin motor domain homology F;124-466/Domain: Kinesin motor domain homology <KMOT>
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                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                                                                      233 VRALEDIL-----LNASSASISVEISYLQLYMETIQDLLAPEKNNISINEDAKTGEVS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKV-----DQRERLA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-----RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PEQPGVI 147
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                                                                                                                                                                                                                                                                                                                                                                                             PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCR-GNIL
                                                                                                                                                                                                                    PARVRVAVRLRPFVDGTAGASD------PPCVRGMDSCSLEIANWRNHQETLKYQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRN----HQETLKYQFDAFYGERST
                                                                                                                                                                             Gaps
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A;Map position: 2
C;Superfamily: kinesin-related protein Eg5; kinesin motor domain homology
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                                                                                                                                                                             42;
                                                                                                                                  Length 1070;
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                                                                                                                                28.0%; Score 525; DB 2; Length 10
35.3%; Pred. No. 1e-33;
tive 69; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDP----
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36.4%; Pred. No. 1.2e-33;
ive 67; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 QQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS----
                                                                                                                            Query Match 28.0%
Best Local Similarity 35.3%
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 36.49
Matches 131; Conservative
Gene: ATSP:F28P10.150
                                                                                                                                                                                                                                                                                                                                                  173
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Cybace: 2-Out-1399 #sequence_revision 22-Out-1399 #text_cnange 16-Aug-2004
RyBoleti, H.; Karsenti, E.; Vernos, I.
Cell 84, 49-59, 1996
A;Title: Kklp2, a new Xenopus centrosomal kinesin-like protein required for centrosome s A;Reference number: 220827; MUID:96140639; PMID:8548825
A;Accession: T30335
A;Accession: T30335
A;Residua; preliminary; translated from GB/EMBL/DDBJ
A;Residuae: 1-1388 -BOLb
A;Cross-references: UNIPROT:Q91785; EMBL:X94082; NID:g1129172; PID:e213754; PIDN:CAA6382
C;Genetics:
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Yorosa

Yandiopsis thaliana

Kineain homolog F28P10.150 - Arabidopsis thaliana

Kineain homolog F28P10.150 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

R;Accelson: Tofo733

R;Reference number: 215793

A;Reference number: 215793

A;Reference to the Protein Sequence Database, April 1999

A;Residon: Tofo73

A;Residon: Tofo73

A;Residues: 1-1070 cQUB>

A;Residues: 1-1070 cQUB>

A;Residues: 1-1070 cQUB>

A;Residues: 1-1070 cQUB>

C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA--- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                   LP2 protein - African clawed frog
;Species: Xenopus laevis (African clawed frog)
;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004
;Accession: T30335
                                        LMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF-RQREGK
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                                                                                                       333 LGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                              Query Match 28.1%; Score 527.5; DB 2; Best Local Similarity .36.5%; Pred. No. 9.3e-34; Matches 126; Conservative 68; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: klp2
C,Superfamily: kinesin motor domain homology
                    273
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Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                       126;
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Best Local S:
Matches 126
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                                                                                                                                                                                                                                                                                                                                                                                            Kinesin-related protein TKRP125 - common tobacco (;Species: Nicotiana tabacum (common tobacco) (;Species: Nicotiana tabacum (common tobacco) (;Species: Se-Reb-1999 #text_change 09-Jul-2004 (;Species: Os-Se-Reb-1999 #text_change 09-Jul-2004 (;Species: T02017 () 170-189; 1997 () 199-189; 1997 () 199-189; 1997 () 199-189; 1997 () 199-189; 1997 () 199-189; 1997 () 199-189; 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 1997 () 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 IREDCRGNILIPGLSQKPISS----PADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 LNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
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252
                                               241
                                                                                                     KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 310
                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VRVAVRIRPFVDGTAGASDPPCVRGMD----SCSLEIANWRNHQETLKYQFDAFYGERS
                                 IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
27.8%; Score 521.5; DB 2; Length 1006;
Best Local Similarity 35.6%; Pred. No. 1.8e-33;
Matches 128; Conservative 69; Mismatches 118; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOODIYAGSVOPILRHLLEGONASVLAYGPTGAGKTHTMLGS---
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: J. 2, X, 7-11; 59-64; 125-132; 222-226, X, 7, 228-230 <COL2>
A; Residues: 2-5, X, 7-11; 59-64; 125-132; 222-226, X, 7, 228-230 <COL2>
C; Complex: heterotrimer of a 115K chain and two kinesin-related chains of Superfamily: kinesin-related protein KTF3; kinesin motor domain homology
C; Keywords ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop
F; 11.348/Domain: kinesin motor domain homology <KMOT>
F; 97-104/Region: nucleotide-binding motif A (P-loop)
F; 97-104/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                    PIDN: AAD24373.1; GSPDB:GNC
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A;Residues: 1-699 <COL1>
A;Cross-references: UNIPROT:P46872; EMBL:L16993; NID:g295245; PIDN:AAA16098.1; PID:g2952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 iFAYGQTGTGKTYTWEGGARKKNGEIPSDAGVIPRAVKQIFDILEAQSAA----EYSLKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
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N,Alternate names: Kinesin-2 chain A; KRP (85/95) 85K chain
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S38982; 872531
R;Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
Nature 366, 268-270, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 TGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 VLAYGPTGAGKTHTMLGS-----PEQPGVIPRALMDLLQLTREEGAEGRPWALSVTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 LPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 STQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 EKGSAKRRTAETLLNKQSSRSHSIFSVTIHIKECTPEGEEIVKSGKLNLVDLAGSENISR
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84687
A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-1076 <STO>
A;Cross-references: UNIPROT:Q9SIB3; GB:AE002093; NID:g4580395; PIDN:AAD2437
C;Genetics: A;Gene: A12g28620
A;Gene: A2g28620
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                            Length 1076;
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37.6%; Pred. No. 3.9e-33;
cive 61; Mismatches 135;
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Indels

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US-10-734-049A-259
US-10-734-049A-259
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Sequence 6, Appli
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Sequence 19691, A
Sequence 18691, A
Sequence 18821, A
Sequence 6841, Ap
Sequence 6841, Ap
Sequence 6841, Ap
Sequence 6859, Ap
Sequence 6860, Ap
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                                                         5, 2004, 18:38:46; Search time 5.60933 Seconds (without alignments) 1056.470 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1878
1 MAAGGSTQQRRREWAAASAA......FYLDTVSALNFAARSKEVIN 370
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Sequence
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1: /cgn2_6/ptodata/2/paa/VBCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/USI1_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/USI1_NEW_COMB.pep:*
      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-10-952-69B-164
US-10-94B-973-2
US-10-94B-973-4
US-10-951-582-4
US-10-951-582-6
US-10-951-582-6
US-10-951-582-8
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US-10-732-923-6904
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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26 95 5.1 912 6 US-10-732-923-424 Sequence 424, App 29 5.1 912 6 US-10-732-923-7145 Sequence 7145, Ap 29 95 5.1 912 6 US-10-732-923-7146 Sequence 7145, Ap 29 95 5.1 912 6 US-10-732-923-7149 Sequence 7147, Ap 31 95 5.1 912 6 US-10-732-923-7149 Sequence 7147, Ap 31 95 5.0 912 6 US-10-732-923-7149 Sequence 7149, Ap 32 94.5 5.0 912 6 US-10-732-923-7149 Sequence 7149, Ap 32 94.5 5.0 912 6 US-10-732-923-679 Sequence 6152, Ap 32 92.5 90 912 6 US-10-732-923-679 Sequence 6152, Ap 32 92.5 90 912 6 US-10-732-923-7198 Sequence 6152, Ap 32 92.5 90 912 6 US-10-732-923-7198 Sequence 7198, Ap 32 90.5 4.8 918 6 US-10-732-923-7198 Sequence 6153, Ap 32 90.5 4.8 918 6 US-10-732-923-6855 Sequence 6153, Ap 40 90 6 US-10-732-923-6855 Sequence 6153, Ap 41 89.5 4.7 819 6 US-10-732-923-6936 Sequence 6157, Ap 42 88.5 4.7 819 6 US-10-732-923-6936 Sequence 6157, Ap 44 88.5 4.7 818 6 US-10-732-923-6936 Sequence 6157, Ap 44 88.5 4.7 818 6 US-10-732-923-6936 Sequence 6157, Ap 45 88.5 4.7 918 6 US-10-732-923-6936 Sequence 6157, Ap 56 US-10-732-923-6936 Sequence 6157, Ap 56 US-10-732-923-6936 Sequence 6158, Ap 56 US-10-732-923-6936 Sequence 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.4%; Score 552.5; DB 6; 39.7%; Pred. No. 1.1e-43; ive 59; Mismatches 114;
                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ITOH, KYOSO
ITOH, FOR THOUSE
TITLE OF INVENTION: TUMOR ANTIGEN
FILE REFERENCE: Q-70382
CURRENT APPLICATION UNMBER: US/10/734,049A
CURRENT FILING DATE: 2003-12-12
PRIOR FILING DATE: 2002-66-11
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 408
SOFTWARE: PATENTIN VERSION 3.3
ALIGNMENTS
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Best Local Similarity 39.7%
Matches 141; Conservative
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                                                                                                                                                                                                                                                    88 -----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTML- 138
                                                                                                                                                                                                                                                                                61 PAPPTRHDFSFDRVFPPGSGQDEVFE-EIAMLVQSALDGYPVCIFAYGQTGSGKTFTMEG 119
                                                                                                                                                                                                                                                                                                                                                                 120 GPGGDPQLEGLIPRALRHLFSVAQELSGGG--WTYSFVASYVEIYNETVRDLLATGTRKG 177
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                                                                                                                                                                                                                                                                                                                                           139 ---GSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPAS--- 192
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7 IRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPP-----TRLSLSRSDERRGTLSGA
                                                                                                                                                                   ----FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK--
                                                                                                                                                                                                58; Gaps
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                                                                               Length 361;
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CURRENT APPLICATION NUMBER: US/10/126,205
PRIOR RAPLICATION NUMBER: US/10/126,205
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2000-11-28
PRIOR PLILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/99/723,595
PRIOR PLILING DATE: 1999-04-20
PRIOR PLILING DATE: 1999-04-20
PRIOR PLILING DATE: 1999-04-20
PRIOR PLILING DATE: US/90/295,612
PRIOR PLILING DATE: US/90/295,612
PRIOR PLILING DATE: US/90/295,612
                                                                             22.5%; Score 423; DB 6; Length 36. 32.8%; Pred. No. 4e-32; ive 59; Mismatches 131; Indels
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Best Local Similarity 32.8%; Pred. No. 4.1e-32;
Matches 121; 'Conservative 59; Mismatches 131;
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GENERAL INFORMATION:
                                                                                 Query Match 22.5
Best Local Similarity 32.8
Matches 121; Conservative
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                      Human
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; TYPE: PRT
; ORGANISM: Ht
US-10-948-973-2
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Sequence 164, Application US/10952698
Sequence 164, Application US/10952698
Sequence 164, Application Sequence 164, Applications and APPLICANT: Mack, David
APPLICANT: Mack, David
APPLICANT: Aziz, Natasha
TITLE OF INVENTION: OF SCREENING FOR MODULATORS OF BLADDER CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/952,698
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 DIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA---L 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 VRVAVRLRPFVD--GTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 NLVDLAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYRDSKLT 321
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                           GLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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SEQUERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
FILE REPERENCE: 1043
CURRENT APPLICATION NUMBER: US/10/948,973
CURRENT PILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US/09/723,595
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 361
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Best Local Similarity 37.24
Matches 128; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                   -10-952-698-164
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 PRCLDMIFNSIGSFQAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQVD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 PEFADMITVQEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLLEEVPFDPIKPKPPQSKLL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 VGVYCRVRPL----GPPD-----QECCIEVINNTTVQLHTPEGYRLNRNGDYKET-Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 494;
                                                                                                                                                                   APPLICANT: Vaiaberg, Eugeni
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION NUMBER: US/10/143.563
PRIOR APPLICATION NUMBER: US/10/143.563
PRIOR PILLING DATE: 2002-05-09
PRIOR PILLING DATE: 2000-11-28
PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
SOFTHARE: FASESEQ FOR Windows Version 4.0
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27.3%; Pred. No. 3.3e-29;
ive 64; Mismatches 127;
                                                                                                                 US-10-951-582-4; Sequence 4, Application US/10951582; GENERAL INFORMATION:
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Best Local Similarity 27.3%
Matches 117; Conservative
                           353 FASKVNQCV 361
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FAEVTOEV 434
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US-10-951-582-6
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                             119 GPGGDPQLEGLIPRALRHLFSVAQELSGQG--WTYSFVASYVEIYNETVRDLLATGTRKG 176
                                                                                                   PAPPTRHDFSFDRVFPPFGSGQDEVFB-EIAMLVQSALDGYPVCIFAYGQTGSGKTFTMEG 119
---GSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPAS--- 192
                                                                         --GDLVIREDCRGN--ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHA 248
                                                                                                                                                   VLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGL-----RLKESGAINTS 300
                                                                                                                                                                           | ::: | :|||||| | 237 VPQLQI-SGEHSSRGLQCGAPLSLVDLAGSE----RLDPGLALGPGERERLRETQAINSS 291
                                                                                                                                                                                                                              LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                                                                                                                                                                                                292 LSTLGLVIMALSNKESHVPYRNSKLTYLLQNSLGGSARALMFVNISPLEENVSESLNSLR 351
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IRVPCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPP-----TRLSLSRSDERKGTLSGA
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Sequence 4, Application US/10948973

Sequence 4, Application US/10948973

Sequence 4, Application US/10948973

SEQUENCE APPLICATION:

TITLE OF INVENTION: Ovel motor proteins and methods for TITLE OF INVENTION: their use

FILE REPERRNCE: 1043

CURRENT APPLICATION NUMBER: US/10/126,205

PRIOR FILING DATE: 2004-09-24

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US/09/723,595

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.5%; Score 423; DB 6; Length 37(32.8%; Pred. No. 4.1e-32; ive 59; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                352 FASKVNQCV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
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139
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US-10-951-582-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.0%; Score 394; DB 6; Length 658; Best Local Similarity 27.3%; Pred. No. 5e-29; Matches 117; Conservative 64; Mismatches 127; Indels 120;
           APPLICANT: Vaisberg, Eugeni
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: Heir use
FILE REFERENCE: 1041
CURRENT FILING DATE: 2004-09-27
PRIOR PPLICATION NUMBER: US/10/951,582
CURRENT FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR APPLICATION NUMBER: US/09/723,630
PRIOR FILING DATE: 2000-11-28
PRIOR PELING DATE: 2000-6-15
PRIOR APPLICATION NUMBER: US/09/314,464
PRIOR FILING DATE: 1099-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASLSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Valaberg, Eugeni
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION NUMBER: US/10/951,582
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FAEVTQEV 434
GENERAL INFORMATION:
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191 PEFADMITVQEFCKABEVDEDSVYGVFVSYIEIYNNYIYDLLEEVPFDPIKPKPPQSKLL 250
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APPLICANT: Wood, Kenneth
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1041
CURRENT APPLICATION UNDER: US/10/951,582
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/143,563
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING LATE: 2000-11-38
PRIOR FILING DATE: 2000-11-38
PRIOR FILING DATE: 2000-11-38
PRIOR PRIOR APPLICATION NUMBER: US/955,424
PRIOR APPLICATION NUMBER: US 09/595,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%; Score 390; DB 6; 27.2%; Pred. No. 6.5e-29; iive 64; Mismatches 127
CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: US/10/143,563

PRIOR FILING DATE: 2002-05-09

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-28

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 1999-05-18

PRIOR PILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: Vaisberg, Eugeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 27.2 Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 PRAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 FAARSKE 367
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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172 VTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRN 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 RIVGATRINORSSRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRIGN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PAREMEKFRVCVRKRPLGMREVRRGEINIITVEDKETLLVHEKKEAVDLTQYILQHVFYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 PAR----VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY-----QF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%; Score 183; DB 6; Length 134;
40.2%; Pred. No. 2.9e-10;
tive 19; Mismatches 49; Indels
                                                                                                          ; Sequence 14884, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT; HYSEQ, INC
; TILLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT PAPLICATION NUMBER: 09/577,409
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR PILING DATE: 2000-05-18
; PRIOR PILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HYSEQ, INC
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
FURENT PRINCE 21272-042
CURRENT PILIOR DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i LOCATION: (1)...(134)
i OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-14894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 26476, Application US/10220366A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-366A-26476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-220-366A-26476
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SEQ ID NO 26476
LENGTH: 134
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LENGTH: 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 MD-----LLQLTREEGAEGRPWALS------VTM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 SYLEIYQEKVLDLL----DPASGDLVIREDC-----RGNILIPGLSQKPISSFADFERH 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 SYIEIYNNYIYDLLEEVPPDPINPNL-HNLNCFVKIKNHNMYVAGCTEVEVKKSTEEAFEV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLPASRNRTVGATRINQRSSRSHAVILVKVDQRERLAP-----FRQRE----GKLYL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 IDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGL-----PRVPYRDSKLTR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 SRSHAVLLVKVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 301
                                                                                                                                                                                                                                                                                                                 16 SGTHAVFQFFLKQQGRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 FVLGKVVDALNQGLPR---VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVS 357
                                                                                                                                                                                              Query Match
19.8%; Score 371; DB 6; Length 960;
Best Local Similarity 27.4%; Pred. No. 1.3e-26;
Matches 110; Conservative 63; Mismatches 118; Indels 110; Gaps
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPRENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
FRIOR APPLICATION NUMBER: 09/577,409
FRIOR PILING DATE: 2000-05-18
FRIOR FILING DATE: 2001-02-38
FRIOR FILING DATE: 2001-02-38
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SOFTWARE: Custom
SOFTWARE: Custom
SOFTWARE: Custom
SOFTWARE: Custom
SOFTWARE: Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: | :: | :: | 394 LFKNYFDGEGKVRMIVCVNPKAEDYEENLQVMRFAEVTQEV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 11.0%; Score 206.5; DB 6; al Similarity 46.2%; Pred. No. 1.9e-12; 55; Conservative 15; Mismatches 44;
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 960
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Matches 55; Conserv
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US-10-220-366A-19691
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Gaps

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RESULT 15
US-10-732-923-6842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 GLRIKESGAINTSLFVLGKVVDAL---NQGLPR------VPYRDSKLTRLLQDSLGG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 LRP----FVD-----FVD------GTAGA---SDPPCVRGMDSCSLEIANWRNHQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 83; Conservative 69; Mismatches 128; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQUENCE 6841, Application US/10732923
GRUERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
FITUE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR SPEQ ID NOS: 24149
NUMBER OF SEQ ID NOS: 24149
LENGTH. 011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 139;
                                                                                                       Sequence 15821, Application US/10220366A

GENERAL INFORMATION:
APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION WUMBER: US/10/220,366A
CURRENT FILING DATE: 2000-08-28
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: CUSTOM
SEQ ID NO 15921
LENGTH: 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1).7.(139)
; OTHER INFORMATION: Xaa = any amino acid or nothing US-10-220-366A-15821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 SAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.3%; Score 174; DB 6; Best Local Similarity 43.2%; Pred. No. 2.1e-09; Matches 41; Conservative 17; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-10-732-923-6841
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
151 LMDLLQ 156
                              121 AKDIFR 126
                                                                                                   US-10-220-366A-15821
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US-10-732-923-6841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 DPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDAEGKVILFIDEIHLVLGAGKTEGSMDA-ANLFKPMLARGOLRCIGATTLEE-YRKYV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 VLLVKVDORERLAPFROREGKLYLID------LAGSEDNRRTGNKGLRLKESGAIN- 298
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                                                                                                134 THIMLGSPEQ--PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEK---VLDLL 188
                                                                                                                                                                                                 189 DPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHA 248
                                                                                                                                                                                                                                                                                                                              325 -----EKDAAFERRFQQVYVAEPSVPDTISILRGLKE-KYEGHHGVRIQDRALINA 374
RHLLEGQNASVLAYGPTGAGK 133
                                                                                                                                                                                                                                   268 EDAEGKVILFIDEIHLVLGAGKTEGSMDA-ANLFKPMLARGQLRCIGATTLEE--YRKYV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
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                               249 VILVKVDORERLAPFROREGKLYLID-----LAGSEDNRRTGNKGLRLKESGAIN-
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6.0%; Score 113; DB 6; Length 911;
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 83; Conservative 69; Mismatches 128; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6842, Application US/10732923

Sequence 6842, Application US/10732923

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCHIC FLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
FRIOR FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 6842
; LENGTH: 911
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     ETLKYQFDAFYGERSTQQDIYAGSVQPIL-
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; ORGANISM: Arabidopsis thaliana
US-10-732-923-6842
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Search completed: November 5, 2004, 19:04:48 Job time : 6.60933 BecB

us-10-797-893-2.rapn

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5, 2004, 18:44:52; Search time 62.7813 Seconds (without alignments) 2081.726 Million cell updates/sec
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1878
1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN
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| cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
| cgn26/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| cgn26/ptodata/2/pubpaa/US08 NEW PUB.pep:*
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| cgn26/ptodata/2/pubpaa/US107 PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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Sequence 80, Appl Sequence 4, Appli Sequence 1228, Ap Sequence 1228, Ap Sequence 320209, Sequence 15901, Sequence 2692, Ap Sequence 2692, Ap Sequence 3708, A Sequence 59708, Sequence 2, Appli Sequence 5, Appli Description 6 US-10-797-893-2 5 US-10-334-143-80 6 US-10-797-893-4 6 US-09-925-300-1228 6 US-10-797-893-8 6 US-10-797-893-8 7 US-10-425-115-320209 6 US-10-437-963-159031 5 US-10-437-963-159031 7 US-10-437-963-103943 US-10-437-963-103943 US-09-883-096-5 ü 8 Length Query 1000.0 1000.0 993.9 933.9 933.9 933.9 933.9 933.9 933.9 933.9 933.9 933.9 933.9 Score 1878 1878 1873 1763 1763 1763 601 597.5 557.5 557.5 544.5 528 12110987654321 Result

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                                                       ORSSRSHAVLLVKVDORERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300
                                                                                                                                              LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
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                                                                                                                                                                                                                                                                                   | Sequence 80, Application US/10334143
| Sequence 80, Application US/10334143
| Publication No. US20040009549A1
| Publication No. US20040009549A1
| GENERAL INPORMATION:
| TITLE OF INVENTION: WITHOUT REMOTE HOMOLOGUES AND NOVEL
| TITLE OF INVENTION: WITHOUT REMOTE HOMOLOGUES AND NOVEL
| TITLE OF INVENTION: WINAES IDENTIFIED WITH THE METHOD
| FILE REFERENCE: 038602/1543
| CURRENT APPLICATION WUMBER: US/10/334,143
| CURRENT FILING DATE: 2002-12-31
| PRIOR PILING DATE: 2001-12-31
| NUMBER OF SEQ ID NOS: 207
| SOFTWARE: PATENTIN VET. 2.1
| SEQ ID NOS: 207
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                                        QEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLN
                                                                                                        241 QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS
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Best Local Similarity 100.
Matches 370; Conservative
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ORGANISM: Homo sapiens
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US-10-334-143-80
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; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFRENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT APPLICATION NUMBER: US/09/724,224
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                    methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%; Score 1873; DB 16;
100.0%; Pred. No. 2.2e-176;
iive 0; Mismatches 0;
Sequence 4, Application US/10797893

Publication No. US20040142397A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel motor proteins and met;
TITLE OF INVENTION: their use
TITLE REFERENCE: 1044
CURRENT APPLICATION UNMERR: US/10/797,893
CURRENT FILING DATE: 2004-01309
PRIOR FILING DATE: 2004-01309
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 512
TYPE: PRI
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Best Local Similarity 100.
Matches 369; Conservative
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US-10-797-893-4
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PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG 203
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                                                                                                                                                                    GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHO
                                                                                                                                      ETLKYQFDAFYGERSTQQD1YAGSVQP1LRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ
                                                                                                                                                                                                                                                                                                                                          NILIPGLSQKPISSFADFERHPLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF
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// Sequence 8, Application US/10797893

// Sequence 8, Application US/10797893

// Publication No. US20040142397A1

// GENERAL INFORMATION:

// APPLICANT: Beraud, Christophe

// TITLE OF INVENTION: Choice motor proteins and methods for TITLE OF INVENTION: their use

// TITLE OF INVENTION: their use

// TITLE OF INVENTION: WOVEL WOOF 107797,893

// CURRENT APPLICATION NUMBER: US/10/797,893

// CURRENT FILING DATE: 2004-03-09

// PRIOR FILING DATE: 2000-11-28

// PRIOR PELING DATE: 2000-11-28

// PRIOR APPLICATION NUMBER: 09/597,292

// PRIOR PELING DATE: 2000-11-28

// PRIOR PERIOR DATE: 2000-11-28

// PRIOR PERIOR DATE: 2000-11-28

// PRIOR PERIOR DATE: 2000-11-28

// PRIOR PERIOR DATE: 2000-11-28

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                               61
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-925-300-1228
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                                                                                                                                                                                                              Length 346;
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; Sequence 1228. Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REPERBNES: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR PILING DATE: 1909-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                         93.9%; Score 1763; DB 16;
100.0%; Pred. No. 9.7e-166;
iive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 346
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Best Local Similarity 100.
Matches 345; Conservative
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Best Local Similarity 99.4
Matches 345; Conservative
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ORGANISM: Homo sapiens
                                                                                                                            , ORGANISM: Human
US-10-797-893-6
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US-09-925-300-1228
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NAME/KEY: SITE
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145

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 159031
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 --YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local Similarity 39.7%; Pred. No. 3.7e-50;
Matches 138; Conservative 69; Mismatches 112; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2692, Application US/10108260A;
Sequence 2692, Application US. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HIELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2592
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29.8%; Score 559; DB 15; Length 548;
Best Local Similarity 38.9%; Pred. No. 4.2e-46;
Matches 132; Conservative 70; Mismatches 121; Indels 16
                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
                                                                                                                                                                                                                                                         LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
, ORGANISM: Homo sapiens
US-10-108-2608-2692
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
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196-10-425-115-320209

1 Sequence 320209, Application US/10425115

1 Sequence 320209, Application No. US20040214272A1

1 Sequence 320209, Application No. US20040214272A1

1 GENERAL INFORMATION:

1 APPLICANT: La Ross, Thomas J.

2 APPLICANT: Zhou, Yihua

2 APPLICANT: Zhou, Yihua

3 APPLICANT: Applicant: Acid Molecules and Other Molecules Associated With

1 TITLE OF INVENTION: No Plants

2 TITLE OF INVENTION: No Plants

3 FILE REFERENCE: 38-21 (53204-28)

CURRENT APPLICATION NOWBER: US/10/425,115

CURRENT APPLICATION NOWBER: US/10/425,115

SEQ ID NO 322209

LENGTH: 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ----SLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSYQPILRHLLEGQNASYLAYG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 MAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSC-
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39.1%; Pred. No. 3.2e-50;
Live 72; Mismatches 113; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 589;
      TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                           ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_55097C.1.Pep
US-10-425-115-320209
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 39.1
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
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331 IEN 333
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US-10-437-963-159031
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301 LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
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US-10-425-114-59708
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
                                                                                                                                                            ; Sequence 59708, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION: APPLICANT: Liu, Jingdong
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526 WADRAKEI 533
                                                         361 FAARSKEV 368
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ORGANISM: Zea mays
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US-10-437-963-103943
                                                                                                                                RESULT 11
US-10-425-114-59708
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Sequence 332919, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongus
APPLICANT: Cao, Yongus
APPLICANT: Cao, Yongus
APPLICANT: OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 332919
LENGTH: 783
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                           154 LLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 213
                                                                                     188 STINAKEIMQLLMKGNRQRTQEPTAANQTSSRSHAVLQVTVRQRSRVKNILQEVRQGRLF 247
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                                                                                                                                                                                                        121 ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY 180
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            YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD
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                                                                                                                                                                                    272 LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL-NQGLPR-VPYRDSKLTRLL
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                                                                                                                                                                                                                                                                  29.7%; Score 557.5; DB 17; 37.0%; Pred. No. 1e-45;
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OTHER INFORMATION: unsure at all Xaa locations
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FEATURE:
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US-10-425-115-332919
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APPLICANT: Ziou, Yihuan
APPLICANT: Ziou, Yihuan
APPLICANT: Kovalit, David K.
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(53313) B
CURRENT PAPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
180
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29.7%; Score 557.5; DB 15; Length 854;
Best Local Similarity 37.0%; Pred. No. 1.1e-45;
Matches 136; Conservative 71; Mismatches 138; Indels 23;
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APPLICANT: APPLICANT:

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197 IREDCRGNILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQ 256
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                                                                                                                                                                                                                                                                                                                                                38 RPPPARVRVAVRLRPFV-----DG-----TAGASDPPCVRGMDSCSLBI
                                                                                                                                                                                                                                                                                                                                                                                 15 RPPTPRELDSQR-RPVVQVVDERVLVFNPEEFDGGFPGLKWGGTHDGPKKKGKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Batel, Umesh A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
TITLE OF INVENTION: NOVEL MOTOR
FILE REFERENCE: 020552-0014009
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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IDENGTH: 383
LENGTH: 383
LENGTH: 383
TYPE: PRAT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HsKip3a
OTHER INFORMATION: Amino acid sequence of HsKip3a fragment used
OTHER INFORMATION: the AFPase assay (Figure 4).
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28.1%; Score 528; DB 9; Length 864;
Best Local Similarity 38.7%; Pred. No. 9.7e-43;
Matches 138; Conservative 46; Mismatches 127; Indels
                                                                                                                                                                                                                                                     Length 383;
                                                                                                                                                                                                                                                        28.1%; Score 528; DB 9; Length 38:
38.7%; Pred. No. 2.9e-43;
tive 46; Mismatches 127; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                      Best Local Similarity 38.7
Matches 138; Conservative
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LENGTH: 864
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                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Li, Fing
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 = 21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 EGVLQGRNGTVFCYGATGAGKTYTMLGTMESPGVMVLAIKDLFTKVRQRSHDGNH---SI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 TMSYLEIYOGKVLDILDPASGDIVIREDCRGNILIPGLSOKPISSFADFERHFLPASRNR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 QLSYLEVYNETVRDILSPGR-PLLIREDKQGTV-AAGLTHYRAYSTDEVMKLLQQGNQNR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 TVGATRINQRSSRSHAVLLVKVDQRE-RLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 TTEPTRVNETSSRSHAILQVIVEYRSIDGGSIVTRVGKLSLIDLAGSERALATDQRIQRS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 KESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 IEGANINRSLALSSCINALVEGKKHIFYRNSKLIQLEKDSLGGSCNTVMIANISPSNLS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDRPCVRGMDSCSLEIANWRNHQETLK------YQFDAFYGERSTQQDIYAGSVQPIL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 GSRSCVKIVNKKDVYLTEFASETDYLKLKRVRGRHFCFDSSFPDTTTQAEVXSTTTSDLV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHILEGONASVLAYGPTGAGKTHTMLGSPEOPGVIPRALMDLLOLTREEGAEGRPWALSV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09883096
; Sequence 5, Application US/09883096
; Patent No. UG20020110883A1
; GENERAL INFORMATION:
; APPLICANT: Bradd, Christophe
; APPLICANT: Sakowicz, Roman
; APPLICANT: Sakowicz, Roman
; APPLICANT: Patel, Umesh A.
; APPLICANT: Davies, Katherine A.
; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
; TILE REPRENCE: 02052-001410US
; CURRENT APPLICATION NUMBER: US/09/883,096
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%; Score 544.5; DB 16; Length 35.3%; Pred. No. 1.9e-44; ive 71; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT4530_101324C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 YLDTVSALNFAARSKEV 368
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          Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 35.3
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
                                                                                      Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CIREK INFORMATION 103943
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US-09-883-096-5
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271 YLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL----NQGLPRVPYRDSKLT 326
                                             262 NLVDLAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYRDSKLT 321
                                                                                                                                                                                 322 FILRDSLGGNAKTAIIANVHPGSRCFGETLSTLNFAQRAKLIKN 365
                                                                                                                                               327 RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
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US-10-332-089-4
                                                                                                                                                                  77 ANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHT 136
                                                                                                                                                                                                                           137 MLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLV 196
                                                                                                                                                                                                                                                                                                                                                                   197 IREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 RERLAPPRO--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 VRVAVRLRPFVD--GTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 DIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA---L 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 SVFATVAKSIVESCMSGYNGTIFAYGQTGSGKTFTWMGPSESDNFSHNLRGVIPRSFEYL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKPISSPADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPF-ROREGKL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 LPR---VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 KGRKTHVPYRDSKLTRLLKDSLGGNCRTYMIAAISPSSLTYEDTYNTLKYADRAKEI 351
                                                                                              15 RPPTPRELDSQR-RPVVQVVDERVLVFNPEEPDGGFPGLKWGGTHDGPKKKGKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10332089
Publication No. US20040072175A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cytokinetics, Inc.
APPLICANT: Baraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth W
APPLICANT: Wood, Kenneth W
APPLICANT: Wood, Renneth W
APPLICANT: Wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/332,089
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: WO PCT/US01/16300
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTTARRE: PATENTIN Ver. 2.1
SEQ ID NO 4
                                  RPPPARVRVAVRLRPFV-
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ORGANISM: Homo sapiens
                                  38
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RESULT 1
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1768
1 MGRCRLSKIGATRRPPPARV.......FYLDTVSALNFAARSKEVIN 346
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/pubpaa/US10D_PUBCOMB.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 6, Appli	Sequence 8, Appli	Sequence 2, Appli	Segmence 80, Appl	Sequence 4, Appli	equence 1228. Ap	Sequence 159031,	Sequence 320209,	Sequence 2692, Ap	Sequence 332919,	Sequence 59708, A	Sequence 103943,	Sequence 5, Appli
	De						S							ഗ
	ai ai	US-10-797-893-6	US-10-797-893-8	S US-10-797-893-2	US-10-334-143-80	US-10-797-893-4	US-09-925-300-1228	US-10-437-963-159031	US-10-425-115-320209	US-10-108-260A-2692	US-10-425-115-332919	US-10-425-114-59708	US-10-437-963-103943	US-09-883-096-5
	08	16	16	16	15	16	6	16	17	15	17	15	16	6
	Query Match Length DB ID	346	487	370	490	512	460	377	589	548	783	854	176	383
de	Query Match	100.0	100.0	99.7	7.66	7.66	99.2	33.8	33.6	31.6	31.1	31.1	30.4	29.9
	Score	1768	1768	1763	1763	1763	1753	597.5	593.5	559	550	550	537	528
	Result No.	-	~	m	4	5	9	7	80	o,	10	11	12	13

Sequence 2, Appli	3	316,			2361		32,	Sequence 2, Appli	164,	Sequence 306, App	142,	1477,	176714		670,	2153,		Seguence 231231,		7903,		Sequence 21903, A	33, A	166	1, App	e 1,	Sequence 23, Appl	11	664,	99	4, App
US-09-883-096-2	5 US-10-220-120-366		5 US-10-332-089-4	5 US-10-332-089-6	4 US-10-369-493-2361	4 US-10-146-473-82	5 US-10-173-999-32	5 US-10-332-089-2	5 US-10-188-832-164	5 US-10-287-226-306	5 US-10-287-226-142	6 US-10-408-765A-1477	6 US-10-437-963-176714	5 US-10-287-226-302	4 US-10-116-712-670	6 US-10-408-765A-2153	5 US-10-334-143-8	US-10	US-10	L7 US-10-739-930-7903	15 US-10-425-114-62748	ΩS	5 US-10-334-143-33	6 US-10-408-765A-1664	US-09-847-874A-1	4 US-10-458-162-1	4 US-10-080-608A-23	4 US-10-370-685-112	4 US-10-116-712-664	4 US-10-116-712-669	US-09-883-096-4
864 9	757 1	757 1	375 1	409 1	774 1	1388 1	1388 1	388 1	388 1	834 1	1401 1	1826 1	1382 1	1115 1	232 1	1232 1	235 1	٦	•	•	•	7	1237 1	672 1	1103 9	1103 1	928 1	928 1	232 1	1232 1	338 9
528 29.9	27 29.8		26 29.8	~	29.8	29.8	29.8	29.8	29.8	29.6	29.5	29.4	29.3	29.3	29.3		18 29.3	.5 29.3	29.3		5 29.1	5 29.0	29.0		28.8	28.8	28.7	28.7	28.7	28.7	504 28.5
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## ALIGNMENTS

US-10-797-893-6	
Sequence 6, Application US/10797893	
GENERAL INFORMATION:	
APPLICANT: Beraud, Christophe	
; TITLE OF INVENTION: their use	
; FILE REFERENCE: 1044	
; CURRENT APPLICATION NUMBER: US/10/797,893	
; CURRENT FILING DATE: 2004-03-09	
; PRIOR APPLICATION NUMBER: US/09/724,224	
; PRIOR FILING DATE: 2000-11-28	
; PRIOR APPLICATION NUMBER: 09/597, 292	
; PRIOR FILING DATE: 2000-06-20	
NUMBER OF SEQ ID NOS: 8	
SOFTWARE: FastSEQ for Windows Version 4.0	
SEQ ID NO 6	
LENGTH: 346	
TYPE: PRT	
; ORGANISM: Human US-10-797-893-6	
100.04;	
Best Local Similarity 100.0%; Pred. No. 1.7e-168; Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0	ö
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Db 1 MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE 60	0
Qy 61 TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQP 120	20
Db 61 TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP 120	20
Qy 121 GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN 180	80

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NUMBER OF SEQ ID NOS: 207
SOFWHARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 490
TYPE: PRT
TYPE: PRT
CRGANISM: Homo sapiens
US-10-334-143-80
Christophe
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 345; Conservative
                                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-10-797-893-2
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                                                                         OREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300
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100.0%; Score 1768; DB 16; Length 487;

Best Local Similarity 100.0%; Pred. No. 2.8e-168;

Matches 346; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                       Sequence 8, Application US/10797893
; Sequence 8, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REPERBRECE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR PILING DATE: 2000-11-28
; PRIOR PLILOR DATE: 2000-11-28
; PRIOR PLILOR DATE: 2000-16-28
; PRIOR PLILOR DATE: 2000-16-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
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US-10-797-893-8
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US-10-797-893-2
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Sequence 80, Application US/2034143
Publication No. US20040009549A1
GENERAL INFORMATION:
APPLICANT: GRIGORLEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR FILING DATE: 2001-12-31
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TITLE OF INVENTION: Novel motor proteins and methods for ITILE OF INVENTION: Novel motor proteins and methods for ITILE OF INVENTION: their use FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT PLING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR PILING DATE: 2000-16-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
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100.0%; Pred. No. 5.9e-168;
tive 0; Mismatches 0;
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LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1228
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                                                                                                                                                              APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAID.
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: GO/124,270
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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 304 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 348
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Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.
                                                                                                             ; Sequence 1228, Application US/09925300; Patent No. US20020151681A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-437-963-159031
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LOCATION: (435)
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**Sequence 4, Application US/10797893

**Publication No. US20040142397A1

**GENERAL INFORMATION:

**APPLICANT: Beraud, Christophe

**TITLE OF INVENTION: Novel motor proteins and methods for

**TITLE OF INVENTION: their use

**TITLE OF INVENTION: their use

**TITLE OF INVENTION: 104-03-09

**CURRENT APPLICATION NUMBER: US/10/724,224

**PRIOR APPLICATION NUMBER: 09/597,292

**PRIOR FILING DATE: 2000-11-28

**PRIOR FILING DATE: 2000-06-20

**NUMBER OF SEQ ID NOS: 8

**SOFTWARE: FastSEQ for Windows Version 4.0

**SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                                                                                            TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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ORGANISM: Human
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                                                                                                                                                                                                                                                       7 PARSSAHLSQPVRVVLRVRPPLSSEAASATAPCV-SLLGCHPGGGVTVQLKD-QHTSRSE 64
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                                                                                            17; Length 589;
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                        Indels
                                                                                     33.6%; Score 593.5; DB 17; 39.2%; Pred. No. 3.2e-50; iive 71; Mismatches 107;
OTHER INFORMATION: Clone ID: MRT4577_55097C.1.pep
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                                                                                                                          Best Local Similarity 39.2%
Matches 135; Conservative
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US-10-108-260A-2692
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             , OTHER INFORMATION US-10-425-115-320209
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US-10-108-260A-2692
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                                    APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 159031
LENGTH: 377
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: AND AND AND AND AND AND APPLICANT: Cao, Yolnyaei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 322209
LENGTH: 589
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33.8%; Score 597.5; DB 16; Length
Best Local Similarity 39.7%; Pred. No. 6.5e-51;
Matches 138; Conservative 69; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
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Sequence 320209, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
             Zhou, Yihua
Cao, Yongwei
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ORGANISM: Oryza sativa
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ORGANISM: Zea mays
FEATURE:
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Fice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 103943
       and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                64 -----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.1%; Score 550; DB 15; Length 8: 38.2%; Pred. No. 1.38-45; Live 68; Mismatches 128; Indels
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US-10-437-963-103943
                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: LIB3689-256-H1_FLI.pep
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TITLE OF INVENTION: Nucleic Acid Molecules an TITLE OF INVENTION: Plants and Uses Thereof FILE REPERENCE: 38-21 (53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NOS: 73128 LENGTH: 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 103943, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 38.29
Matches 132, Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Avoid K.
APPLICANT: Avoid M.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322) B
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
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LENGER OF SEQ ID NOS: 369326
LENGER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.1%; Score 550; DB 17; Length 783; Best Local Similarity 38.2%; Pred. No. 1.1e-45; Matches 132; Conservative 68; Mismatches 128; Indels 1
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                          ODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                             Sequence 332919, Application US/10425115
Publication No. US20040214272A1
                                                                                                                                                                                                                            GENERAL INFORMATION:
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ORGANISM: Zea mays
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US-10-425-114-59708
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RESULT 15
US-10-220-120-366
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                                                                                                                                                                                                                                        LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 189
                                                                                                                                                                                                                                                                                                                                                                      PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRB-RLAPFRQREGKLYL 248
                                   SRIMVFVRLRPMSRKEKDAGSRSCVKIVNKKDVYLTEFASETDYLRLKRVRGRHFCFDSS 263
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                                                                                                                       IDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDS
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Fatent No. US20020110883A1
GENERAL INFORMATION:
APPLICANT: Braud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Standarew
APPLICANT: Standarew
APPLICANT: Patel, Umesh A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REPERENCE: 020552-00141008;
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
FRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 383;
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ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||| ::::||||:| ::|||:||:||:||:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
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LENGTH: 383
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US-09-883-096-5
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233 RERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQG 290
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                                                                                                                                                                                                                      291 LPR----VPYRDSKLTRLLODSLGGSAHSILLANIAPERRFYLDTVSALNFAARSKEV 344
                                                                                                                                                                                                                                                     295 KGRKTHVPYRDSKLTRLLKDSLGGNCRTVMIAAISPSSLTYEDTYNTLKYADRAKEI 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 ANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHT
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APPLICANT: Graven, Andrew
APPLICANT: Graven, Andrew
APPLICANT: Yu, Ming
APPLICANT: Yu, Ming
APPLICANT: Backwicz; Roman
APPLICANT: Backwicz; Roman
APPLICANT: Backwicz; Roman
APPLICANT: Backwicz; Romen
APPLICANT: Backwicz; Romen
APPLICANT: Backwicz; Romen
APPLICANT: Backwicz; Romen
APPLICANT: Backwicz; Romen
APPLICANT: Backwicz; Romen
APPLICANT: WOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT APPLICATION NUMBER: US 09/594,655
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR APPLICATION NUMBER: US 09/594,655
SPRIOR PRILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
LENGTH: 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino acid sequence encoded by human kinesin motor OTHER INFORMATION: proctein gene Hakip3a (Figure 1).
OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of HsKip3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09883096; Patent No. US20020110883A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 RPPPARVRVAVRLRPFV-----
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Best Local Similarity 38.7
Matches 138; Conservative
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120 TGSGKSYTWMGTADQPGLIPRLCSGLFERTQKE--ENEEQSFKVEVSYMEIYNEKVRDLL 177
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               11 LGGCRMG------DSKVKVAVRIRP-MNRRETDLHTKCVVDVDANKVILNPVNTNLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 HAVLLVKVDQRERLAPFR-----QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL
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Job time: 59.709 secs
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; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:403409.1.orf3:2000MAY19
US-10-220-120-366
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APPLICANT: LINCOLN, Stephen B.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
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Sequence 366, Application US/10220120
Publication No. US20040048253A1
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RUSSO, Frank D.
STOCKDREHER, Theresa K.
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DAHL, Christopher R.
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
                                                                                                                                                                                           PANZER, SCOCT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHANG, Simon C.
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YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
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OSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEN, Alice
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US-09-724-224-6

i Sequence 6, Application US/09724224

i Sequence 6, Application US/09724224

j Rement No. 6387644

j GENERAL INFORMATION:

i APPLICANT: Beraud. Christophe

i TITLE OF INVENTION: their use

i TITLE OF INVENTION: their use

i TITLE OF INVENTION NUMBER: US/09/724,224

CURRENT APPLICATION NUMBER: US/09/724,224

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR PRIOR PILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 346
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CRGANISM: Human
US-09-724-224-6
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   us-lu-us-sl. Application US/10093317;
Patent No. 6762043;
GENERAL INPORMATION:
TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: Lteir use FILE REFERENCE: 104.
TITLE OF INVENTION: Lteir use FILE REFERENCE: 104.
CURRENT FILING DATE: 2002-03-06;
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR PLICH DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PRASEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 346
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| Sequence 8, Application US/09724224 |
| Sequence 8, Application US/09724224 |
| Sequence 8, Application US/09724224 |
| Sequence 9, Application US 638764 |
| Tarent No. 6387644 |
| TITLE OF INVENTION: No. 6387644el motor proteins and methods for 1TILE OF INVENTION: Lheir use |
| TITLE OF INVENTION: Lieir use |
| TITLE OF INVENTION: 2000-11-28 |
| CURRENT FILING DATE: 2000-11-28 |
| PRIOR APPLICATION NUMBER: 09/597,292 |
| NUMBER OF SEQ ID NOS: 8 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NOS 8 |
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100.0%; Score 1768; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-180;
Matches 346; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Human
US-09-724-224-8
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; ORGANISM: Human
US-10-093-317-6
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100.0%; Score 1768; DB 3; Length 487; 100.0%; Pred. No. 2.1e-180;

Query Match Best Local Similarity

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; Sequence 8, Application US/10093317
; Patent No. 6762043
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT FLILMG DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR PTLING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FRAESEQ for Windows Version 4.0
; SEQ ID NO 9.
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TYPE: PRT
ORGANISM: Human
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US-09-724-224-4

i Sequence 4, Application US/09724224

i Sequence 4, Application US/09724224

i Batch No. 6387644

i GENERAL INFORMATION:

i APPLICANT: Beraud, Christophe

i TITLE OF INVENTION: No. 638764el motor proteins and methods for TITLE OF INVENTION: their use

i FILE REFERENCE: 1044

i CURRENT APPLICATION NUMBER: US/09/724,224

i FRIOR APPLICATION NUMBER: 09/597,292

i RIOR FILING DATE: 2000-01-28

i NUMBER OF SEQ ID NOS: 8

i SOFTMARE: PastSEQ for Windows Version 4.0
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100.0%; Pred. No. 7.6e-180;
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ORGANISM: Human
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                                                                                                                         ; Sequence 2, Application US/09724224; Sequence 2, Application US/09724224; Patent No. 6387644; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe; TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use; FILE REPERBYCE: 1044; CURRENT FILING DATE: 2000-111-28; PRIOR APPLICATION NUMBER: 09/597,292; PRIOR FILING DATE: 2000-06-20; NUMBER OF SEQ ID NOS: 8; SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6762043
GENERAL INFORMATION:
TATLE OF INVENTION: No. 6762043el motor proteins and methods for 1TILE OF INVENTION: their use
TITLE OF INVENTION: their use
TITLE APPLICATION NUMBER: US/10/093,317
CURRENT APLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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99.7%; Score 1763; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.5e-180;
Matches 345; Conservative 0; Mismatches 0; Indels
326 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
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LENGTH: 370
TYPE: PRT
ORGANISM: Human
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US-09-724-224-2
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TYPE: PRT
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267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
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                                                                                                                                             Sequence 4, Application US/10093317;
Sequence 4, Application US/10093317;
Parent No. 6762043;
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for TITLE OF INVENTION: their use
TITLE OF INVENTION: their use;
FILE REFERENCE: 1040.
FILE REPERENCE: 1040.
PRIOR APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2002-03-06;
PRIOR PILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 512
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Sequence 35, Application US/09595684B

Patent No. 6544766

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Sakowicz, Roman

APPLICANT: Sakowicz, Roman

APPLICANT: Wood, Kenneth

APPLICANT: Yu, Ming

TITLE OF INVENTION: Human kinesins and methods of producing

TITLE OF INVENTION: and purifying human kinesins

PILE REFERENCE: Cytop036

CURRENT APPLICATION NUMBER: US/09/595,684B
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                                                               Similarity
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ORGANISM: Human
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US-09-595-684B-35
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Best Local Simi
Matches 345;
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60 ETLKYOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 119
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; Sequence 4, Application US/09724511
; Sequence 4, Application US/09724511
; Patent No. 6391601
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6391601e1 motor proteins and methods for
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: 009/09/124,511
; CURRENT APPLICATION NUMBER: US/09/724,511
; CRRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/632,344
; MINDER OF FILING DATE: 2000-08-03
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Best Local Similarity 39.0%; Pred. No. 4.6e-50;
Matches 141; Conservative 59; Mismatches 114; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 665
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milarity 100.0%;
Conservative 0;
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Best Local Similarity
Matches 345; Conserv
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ORGANISM: Human
                                                                                                                                                            TYPE: PRT
ORGANISM: Human
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60 ETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 119
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                                                                                                                                                                                                                                                               APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6534309el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/632,344
CURRENT APPLICATION NUMBER: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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; Patent No. 6391601
; GENERAL INFORMATION:
GAPLICANT: Beraud, Christophe
TITLE OF INVENTION:
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/724,511
; CURRENT APPLICATION NUMBER: 09/632,344
; PRIOR FILING DATE: 2000-08-03

    Score 549; DB 4; Length 355;
    Pred. No. 4.6e-50;
    Mismatches 114; Indels

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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                               ; Sequence 4, Application US/09632344; Patent No. 6534309; GENERAL INFORMATION:
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Best Local Similarity
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TYPE: PRT
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                       353
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                                                                                                                                                                                                                                                                                                                                                                                                                                               296 CFQRKNQ---HIPYRNSKLTRLLKDSLGGNCQTIMIAAVSPSSVFYDDTYNTLKYANRAK 352
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6492151el motor proteins and methods for
TITLE OF INVENTION: Lets use
FILE REFERENCE: 1046
CURRENT PRINCION NUMBER: US/09/723,097
CURRENT PLING DATE: 2000-11-27
PRIOR PRINCI DATE: 2000-11-27
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS:
SOFTWARE: FASELSEQ for Windows Version 4.0
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39.0%; Pred. No. 4.6e-50;
tive 59; Mismatches 114; Indels
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LENGTH: 355
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US-09-723-097-4.
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US-09-632-344-2
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                                                                                                                                                         Length 367;
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39.0%; Pred. No. 4.9e-50;
iive 59; Mismatches 114;
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TITLE OF INVENTION: 1046
CURRENT APPLICATION WUMBER: 09/632,344
RICHARD ATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4000-08-03
NUMBER OF SEQ ID NOS: 4000-08-03
SEQ ID NO S: 580 ID NO S: 4000-08-03
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US-09-723-097-2
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                                                                     ; TYPE: PRT
; ORGANISM: Human
US-09-724-511-2
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LENGTH: 367
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                                                                                    186 GVVVHGLTLHQPKSS--EBILHLLDNGNKNRTQHPTDMNATSSRSHAVFQIYLRQQDKTA
                                                                                                                                                 238 PFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL-----
                                                           180 NILIPGLS-QKPISSFADFERHFLP-ASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-632-344-2

15 Sequence 2, Application US/09632344

15 Sequence 2, Application US/09632344

15 Sequence 2, Application US/09632344

15 Sequence 3, Application US/09632344

15 SEPLICANT: Beraud, Christophe

17 TLLE OF INVENTION: No. 653430991 motor proteins and methods for TITLE OF INVENTION: their use

17 TLLE OF INVENTION: their use

18 TLE REFERENCE: 1046

19 CURRENT APPLICATION NUMBER: US/09/632,344

10 CURRENT FILING DATE: 2000-08-03

10 NUMBER OF SEQ ID NOS: 4

11 SOFTWARR: PastSEQ for Windows Version 4.0

11 SEQ ID NO 2

12 LENGTH: 367
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Search completed: November 5, 2004, 18:46:46 Job time : 14.5172 secs

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US-09-724-224-8

i Sequence 8, Application US/09724224

i Sequence 8, Application US/09724224

i Sequence 8, Application US/09724224

i GENERAL INFORMATION:

i APPLICANT: Beraud, Christophe

i TITLE OF INVENTION: No. 6387644e1 motor proteins and methods for

i TITLE OF INVENTION: their use

i TITLE OF INVENTION: their use

i CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-01-28

i PRIOR APPLICATION NUMBER: 09/597,292

i PRIOR FILING DATE: 2000-06-20

i WUMBER OF SEQ ID NOS: 8

i SOFTWARE: FastSEQ for Windows Version 4.0

i SEQ ID NO 8
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US-09-632-344-4
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US-09-723-097-2
US-09-632-344-2
US-09-162-373-1
US-09-162-373-1
US-09-162-373-1
US-09-123-256-1
US-09-723-256-6
US-09-723-219-6
US-09-723-219-6
US-09-723-219-6
US-09-724-519-6
US-09-592-037-6
US-09-428-1568-2
US-09-428-1568-2
US-09-428-1568-2
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US-09-428-1568-2
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US-09-541-782-10
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US-09-724-224-8
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Sequence 4, Al
Sequence 35, 2
Sequence 6, Al
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Sequence 8,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-093-317-8

US-10-093-317-4

US-10-093-317-4

US-10-093-317-4

US-10-093-317-6

US-10-093-317-6

US-10-093-317-2

US-09-724-224-6

US-09-724-224-6

US-09-592-054-4

US-09-592-054-6

US-09-592-054-6

US-09-592-054-6

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US-09-883-096-2
US-09-724-511-4
US-09-723-097-4
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ORGANISM: Human
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Patent No. 6762043
General INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2002-03-06
PRIOR PILING DATE: 2000-11-28
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; Pred. No. 1.1e-225;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 487
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Best Local Similarity 100.0%;
Matches 487; Conservative 0;
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Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 486; Conservative 0; Mismatches 0;
Sequence 4, Application US/09724224;
Patent No. 6387644;
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6387644el motor prot:
TITLE OF INVENTION: their use
FILE REFREENCE: 1044;
CURRENT APPLICATION NUMBER: US/09/724,224;
CURRENT FILING DATE: 2000-11-28;
PRIOR APPLICATION NUMBER: 09/597,292;
PRIOR FILING DATE: 2000-06-20;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-033-317-4
IS-10-033-317-4
; Sequence 4, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor prot
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
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                                                                                                        tch 99.8%; Score 2467; DB 4; I al Similarity 100.0%; Pred. No. 5.6e-225; 486; Conservative 0; Mismatches 0;
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71.5%; Score 1768; DB 3;
Best Local Similarity 100.0%; Pred. No. 4e-159;
Matches 346; Conservative 0; Mismatches 0;
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Sequence 6, Application US/09724224

Patent No. 6387644

GENERAL INPORMATION:

TITLE OF INVENTION: No. 6387644el motor prot.

TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FREESEQ FOR WINGOWS VERSION 4.0
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          ; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-35
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; ORGANISM: Human
US-09-724-224-6
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                                                                                                          Query Match
Best Local S:
Matches 486
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Fatent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
TITLE OF INVENTION: UNBER: 09/295,612
FILE REFERENCE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                              Length 512;
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99.8%; Score 2467; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 486; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Human
US-10-093-317-4
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Sequence 2, Application US/09724224
Patent No. 6387644
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Best Local Similarity 100.
Matches 345; Conservative
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LENGTH: 370
TYPE: PRT
ORGANISM: Human
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US-09-724-224-2
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US-10-093-31,7-2
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                                                              61 TLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP 120
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6762043e1 motor proteins and methods for
TITLE OF INVENTION: Lenir use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: 08/10/093,317
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/724,224
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 4e-159;
tive 0; Mismatches 0; Indels
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Patent No. 6762043
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Best Local Similarity 100.
Matches 346; Conservative
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US-10-093-317-6
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TYPE: PRT
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US-10-093-317-6
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Sequence 2, Application US/10093317

Patent No. 6762043

GENERAL.INFORMATION:

APPLICAMT: Beraud, Christophe

TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/10/093,317

CURRENT FILING DATE: 2002-03-06

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR PILING DATE: 2000-06-20
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100.0%; Pred. No. 1.3e-158;
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100.0%; Pred. No. 1.3e-158;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
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Best Local Similarity
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	RESULT 11 US-09-592-054-4 ; Sequence 4, Application US/09592054 ; Fatent No. 6440684 ; GENERAL INFORMATION: ; APPLICANT: Beraud, Christophe ; APPLICANT: Finer, Jeffrey ; APPLICANT: Sawwicz, Roman ; APPLICANT: Wood, Kenneth	TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: THE PERENCE: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF OR THE COURSE OF ORGANISM: TYPE: PRT ORGANISM: Human -09-592-054-4 Query Match  1 MGRCKLSKIGATRRPPPARVRVAVRLRPFVDGTAGASD	OY 19 POUVEGENES LEARNWINHQUE THE RESTROCHES OF POUNCE TO STAND THE LEAGURE OF THE LANDRARK INNERLY OF THE LEAGURE OF THE LANDRARK INNERLY OF THE LEAGURE OF THE LEAGURE OF THE LEAGURE OF THE LANDRARK INNER OF THE LEAGURE OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INNER OF THE LANDRARK INN
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APPLICANT: Braud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPRENCE: 1016
CURRENT APPLICATION UNBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
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RESULT 13 US-09-592-054-2 ; Sequence 2, Application US/09592054

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Sequence 2, Application US/09572191

Sequence 2, Application US/09572191

Sequence 2, Application US/09572191

Sequence 2, Application Gassafele

Sequence 3, Application

APPLICANT: Baraud, Christophe

APPLICANT: Sakowicz, Roman

APPLICANT: Sakowicz, Roman

APPLICANT: Wood, Kenneth

TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REPERENCE: 1017

CURRENT APPLICATION UNMBER: US/09/572,191

CURRENT PILING DATE: 2000-05-17
APPLICANT: Finer, Jeffrey
APPLICANT: Finer, Jeffrey
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
CURRENT APPLICATION WUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
ANDRER OF SEQ ID NOS: 8
ANDRER OF SEQ ID NOS: 8
ANDRER OF SEQ ID NOS: 8
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22.7%; Score 561.5; DB 4; Length 1232;
Best Local Similarity 32.0%; Pred. No. 8.3e-44;
Matches 158; Conservative 97; Mismatches 163; Indels 75;
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LENGTH: 123
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                                                                                                                        ; Score 561; DB 3; Length 13; Pred. No. 1.1e-43; 97; Mismatches 192; Indels
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Fatent No. 6379912
GENERAL INFORMATION:
APPLICANT: Baraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6379912e1 motor proti
TITLE OF INVENTION: their use
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/723,262
CURRENT FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1388
                                                                                                                         22.7%;
                                                                                                                        Query Match
Best Local Similarity 30.9*
Matches 162; Conservative
                                                         ; TYPE: PRT
; ORGANISM: Human
US-09-572-191-2
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22.7%; Score 561; DB 3; Length 1388;

Query Match

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al Similarity 30.9%; Pred. No. 1.1e-43; 162; Conservative 97; Mismatches 192; Indels
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| Cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.ppp:*
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| Cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.ppp:*
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| Cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/US00 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/US00 NEW PUB.ppp:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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2472
                                 Copyright
                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 8, Appli	Sequence 4, Appli	Sequence 80, Appl	Sequence 1228, Ap	Sequence 6, Appli	Sequence 2, Appli	Sequence 320209,	Sequence 159031,	Sequence 33, Appl	Sequence 670, App	Sequence 2153, Ap	Sequence 8, Appli	Sequence 103943,
SOFTWAKEES		ΙD	US-10-797-893-8	US-10-797-893-4	US-10-334-143-80	US-09-925-300-1228	US-10-797-893-6	US-10-797-893-2	US-10-425-115-320209	US-10-437-963-159031	US-10-334-143-33	US-10-116-712-670	US-10-408-765A-2153	US-10-334-143-8	US-10-437-963-103943
		DB	16	16	15	6	16	16	11	16	15	14	16	15	16
	* Query	Length	487	512	490	460	346	370	589	377	1237	1232	1232	1235	116
	Query	Match	100.0	99.8	93.4	96.6	71.5	71.3	24.6	24.3	23.4	23.2	23.2	23.2	23.1
		Score	2472	2467	2309	2141	1768	1763	608	601	578.5	574.5	574.5	574.5	571
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Sequence 332919, Sequence 59708, A Sequence 2692, Ap Sequence 231231, Sequence 82, Appl Sequence 32, Appl		Sequence 314, App Sequence 316, App Sequence 316, App Sequence 2, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	
US-10-428 US-10-428 US-10-108 US-10-429 US-10-146 US-10-173	US-10-332-089-25 US-10-332-089-216 US-10-188-832-16 US-10-287-226-14 US-10-425-114-62 US-10-408-765A-1	US-10-287-212-305 US-10-287-2126-314 US-10-363-829-316 US-09-883-096-2 US-09-847-874A-1 US-10-408-765A-1477	0210-1100244
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## ALIGNMENTS

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121 GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN 180
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Sequence 8, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: 000461
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2000-11-28
; PRIOR PILING DATE: 2000-11-28
; PRIOR PILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FRSEEQ for Windows Version 4.0
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ilarity 100.0%; Pred. No. 9.3e-202;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 487; Conserv
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267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 326
                                                                                                                                                                                                                                                                                    Sequence 80, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: GUDARGANAM, SUCHA

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

FILE REFERENCE: 038602/1543

CURRENT PAPLICATION NUMBER: US/10/334,143

CURRENT PALLING DATE: 2002-12-31

PRIOR APPLICATION NUMBER: 66/343,169

PRIOR FILING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 207
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                                                                                                                                        IDRILIASOGSOGAPLLSTPKRERWYLWKTVEEKDLEIERLKTKOKELEAKMLAOKAEEKE
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                                         TRILLODSIGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens US-10-334-143-80
                                                                                                                                                                                                NHCPTM 487
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US-10-334-143-80
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LENGTH: 490
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                                                             GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN
                                               ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
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TITLE OF INVENTION: Novel meter proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT APPLICATION NUMBER: US/09/724,224
PRIOR PILING DATE: 20004-03-09
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.8%; Score 2467; DB 16; Best Local Similarity 100.0%; Pred. No. 2.7e-201; Matches 486; Conservative 0; Mismatches 0;
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Publication No. US20040142397A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ENHCPIM 487
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US-10-797-893-4
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US-10-797-893-4
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241 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNGGLPRVPYRDSK 300
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                                                                             Sequence 6, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT BEARING, Christophe
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT PLILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFFWARE PARENCE : 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFFWARE FASESEQ for Windows Version 4.0
; SEQ ID NO 6
; SEQ ID NO 6
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Sequence 2, Application US/10797893

Publication No. USZ0040142397A1

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: Novel motor proteins and methods for

TITLE OF INVENTION: Hoir use

FILE REFERENCE: 104

CURRENT FILING UNTE: 2004-03-09

PRIOR PPLICATION NUMBER: US/09/724,224

PRIOR PLILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE PRESENCE OF Windows Version 4.0

SEQ ID NO: 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.5%; Score 1768; DB 16;
100.0%; Pred. No. 5.8e-142;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
COCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LKYQFDAFYGEXSTQQDIYAGSVQPILRHLLEGQNASVLAYGFTGAGKTHTMLGSPEQPG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHALGP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 VKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLQ 423
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                                                                                                                                         Sequence 1228, Application US/09925300
Fatent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SEQ ID NO 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.6%; Score 2141; DB 9; Length 46 Best Local Similarity 95.9%; Pred. No. 1.4e-173; Matches 422; Conservative 1; Mismatches 17; Indels
                          454 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDL 488
422 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                              US-09-925-300-1228
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APPLICANT: Li, Ping,
APPLICANT: Li, Ping,
APPLICANT: Li, Ping,
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                         ---KELLGP----PEAKRARGPEEEIGSPEPMAAP-----ASASOKLSPLOKLS 409
                                                                                                                                                                                                                                                                                                 408 KIKKILFDPVVHVPTENIPREHRQTEVNTPKKVVLPSVTPCNEKHEASLRKALSPIS--S 465
                                                                                                                                                                                                                                                                                                                                               SWDPAMLERLLSLDRLLASQGSQGAPLL---STPKRERMVLMKTVEEKDLE-IERLKTKQ 465
                                                                                                                                                                                                                                                                                                                                                                    RLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFINESLQP----- 356
                                                                                                                                                  DMEAKLRAWLESKGKTKSIQRMDGLFSPIASKTPLSVSHWKQPTSSRIPCRVKAMDQDGG 407
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EGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLT
                                                                          Gaps
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US-10-437-963-159031
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 KEALVOOYLDLLNVANKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.7%
Matches 151; Conservative
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ORGANISM: Oryza sativa
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APPLICANT:
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Sequence 320209, Application US/10425115
Sequence 320209, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A ROSS, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Youngein TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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24.6%; Score 608; DB 17; Length 589;
Best Local Similarity 31.1%; Pred. No. 1e-42;
Matches 174; Conservative 94; Mismatches 163; Indels 128; Gaps
                                                                                                                                                                                         26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQGT
                                                                                                                                                                                                                                                                                                                            2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQET
                                                                                                                          Gaps
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                                                                                       Length 370;
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US-10-425-115-320209
                                                                                       Query Match 71.3%; Score 1763; E
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 345; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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LENGTH: 589
                      ; TYPE: PRI
; ORGANISM: Hum
US-10-797-893-2
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                         65 QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS----PEQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 VPXRDSKLTRILQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKPIVNID 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 LQPHALGPVK--LSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSP-LQKLSS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 PQTAELNHLKOQVQQLQVL----LLQAHGG------TLPGSITVEPSENLQSLME 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 MDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 PTVGVIPR----VIQLLFKEIDKKSDFEFTLKVSYLEIYNEEILDLLCPSREKAQINIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 LAPPROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--
     119 LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-ELEAKMLAQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                    APPLICANT: Switzer, Ann
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.568
CURRENT APPLICATION NUMBER: US/10/116,712
CURRENT FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 670
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%; Score 574.5; DB 14; Length 32.5%; Pred. No. 2.2e-39; ive 97; Mismatches 161; Indels
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US-10-408-765A-2153
; Sequence 2153, Application US/10408765A
                                                                                                                                                                                                            ; Sequence 670, Application US/10116712; Publication No. US20030194764A1; GENERAL INFORMATION: APPLICANT: Bangur, Chaitanya S.
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DLOKLVETLEDQE 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.59
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                        LEDQE 461
                                                                              477 AEEKE 481
                                                                                                                                                                        RESULT 10
US-10-116-712-670
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 670
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                                                                                                                                   221 VKGKLNLITSXDLAGNEDNRRTCNEGIRLQESAKINQSLFALSNVISALNKKEPRIPYRE 280
                                                                                                                                                                                        SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA 358
                                                                                                                                                                                                            281 SKLTRILQDSLGGNSHAVMIACLNPVE--YQEAVHTVSLAARSRHVTN-------HM 328
LMXSTVLALCTGT-----WC-SVEISYYEVYMERCYDLLEPKAREIMVLDDKDGNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDPCTEQEEVFNKAVAPLIKGIFKGYNATVLAYGQTGSGKTYSMGGAYTAEQENEPTVGI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQP--GV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIREDCRGN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 240
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                                                              LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                           242 REGKLYLI----DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD
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APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOWOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
FRIOR APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 60/343,169
RIOR PILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PARCHIN Ver. 2.1
SEQ ID NO 3322
                                                                                                                                                                                                                                                                                      329 SSASKXKDKVDM---BAKLRAWLESKGKTKSIQRMDGLLSPNAIKTPLSMSQ 377
                                                                                                                                                                                                                                                                 359 LGPVKLSQKELLGPPEAK-----RARGPEE-----EEIGSPEPMAAPASASQ 400
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Pred. No. 1e-39;
7; Mismatches 172; Indels 59;
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Publication No. US20040009549A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 119
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Publication No. US20040009549A1
GENERAL INFORMATION:
APPLICANT: GRIGORLEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
                                                                  APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Tylor, Steven W.
APPLICANT: Marnock, Dale E.
ITILE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408, 765A
CURRENT APPLICATION NUMBER: 2033-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 2153
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

23.2%; Score 574.5; DB 16; Length 1232;
Best Local Similarity 32.5%; Pred. No. 2.2e-39;
Matches 160; Conservative 97; Mismatches 161; Indels 75;
Publication No. US20040101874A1
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                 GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo sapiens
US-10-408-765A-2153
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION DIADE: 204966
SEQ ID NO 103943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 VPYRDSKLTRILQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKRIVNID 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 LQPHALGPVK--LSQKELLGPPEAKRARGPEEEEIGSPEPWAAPASASQKLSP-LOKLSS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 MDPAMLERLISLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-EL 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P--GVIPRALMDLLQLTREEGAEGREWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES
                                                                                                                                                                                                                                                                                                                                                                                              20 VRVAVRLRP------FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY
                                                                                                                                                                                                                                                                                                Query Match
23.2%; Score 574.5; DB 15; Length 1235;
Best Local Similarity 32.5%; Pred. No. 2.2e-39;
Matches 160; Conservative 97; Mismatches 161; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VRVALRCRPLVPKEISEGCQMCLSFVPG-----EPQVVVGTDK----
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION UNMER: 60/343,169
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SEQ ID NO 8
LENGTH: 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-437-963-103943

i. Sequence 103943. Application US/10437963

i. Publication No. US20040123343A1

; GENERAL INFORMATION:
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449 DLQKLVETLEDQE 461
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US-10-334-143-8
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRINCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO S9708
LENGTH: 854
                                                                                                                                    119 OPGVIPRALMDILQLTREEGAEGRPWALSVTMSYLEIYQEKVLDILDPASGDLVIREDCR 178
                                                                                                                                                                                                                                                                                                 317 NPGVMVLAINDLFSKVTQKNH-----SIKLSYLEIYNETVRDLLSPGS-PLNLREDKQ 368
                                                                                                                                                                                                                                                                                                                                                                                                                                        355 -QPHALGPVKLS-QKE--LLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 MDPAMLERLLSLDRLLASQGSQGAPLLS----TPKRERMVLMKTVEEKDLEIERLKTKQK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV---INRPFTNESL- 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KIGA-TRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK--- 63
                                                                                                            8 KIGA-TRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---
                                                                                                                                                                                                                                                                                                                                                              | |: ||:|| || | |: | 369 G-IVAAGLIQRSVYSTDEVMELLQKGNKNRTTEPTRVNETSSRSHAVLQVVVEYRSLDGV
                                                                                                                                                                                                                                                                                                                                        GNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAP
                                                                                                                                                                                                                                                                                                                                                                                                                239 FROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPE
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                                        Length 783;
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33.6%; Pred. No. 2.5e-39;
tive 91; Mismatches 195; Indels
                                                                           Indels
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US-10-425-114-59708
                                    Query Match 23.1%; Score 571; DB 17; Best Local Similarity 33.6%; Pred. No. 2.2e-39; Matches 163; Conservative 91; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 59708, Application US/10425114; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.6%
Matches 163; Conservative
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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US-10-425-115-332919
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Publication No. US20040214272A1
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: E. ROSA, Thomas J.
APPLICANT: E. ALOA, YALUA
APPLICANT: ZLOA, YALUA
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: 105/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 332919
LENGTH: 783
                                                                                                                                                                                                                                                                                129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619 ILAGN-----CFNTPDSKRPAAENAQVRDLQRKVKAMEAEIEKMK-KEHLLQLK---Q 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LL-----GPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 RAYSTDEVMKILLQCGNQNRTTEPTRVNETSSRSHALLQVIVEXRSIDGGSIVTRVGKLSL
                                                                                                                                                                                                                         18 ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK-----YQFDAF
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                                                                                                                              Length 776;
                                                                                                                          23.1%; Score 571; DB 16; Length 7 llarity 31.5%; Pred. No. 2.2e-39; Conservative 99; Mismatches 194; Indels
                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101324C.1.pep
US-10-437-963-103943
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: WRT4577_66737C.1.pep
               TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                            Similarity
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ORGANISM: Zea mays
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Best Local Sim:
Matches 152;
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64 -----YOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPE 118
                                                 388 NPGVMVLAINDLFSKVTQKNH-----SIKLSYLEIYNETVRDLLSPGS-PLNLREDKQ 439
                                                                                                                                   179 GNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAP 238
                                                                                                                                                                                                    355 -QPHALGPVKLS-QKE--LLGPPEAKRARGPEEERIGSPEPMAAPASASQKLSPLOKLSS 410
                                                                                                                                                                                                                                                                                                    268 EVGAGTAEAAESRILVFVRLRPMSRKEKEAGSRSCVKIVNRKEVFLTESASENDYLRLKR 327
                                                                                     119 OPGVIPRALMDILQLTREEGAEGRPWALSVTMSYLRIYORKVLDLLDPASGDLVIREDCR 178
                                                                                                                                                239 FROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD 298
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Search completed: November 5, 2004, 19:09:49 Job time : 83.6338 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
          Copyright
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- protein search, using sw model OM protein

5, 2004, 18:34:12; Search time 14.1983 Seconds (without alignments) 3300.235 Million cell updates/sec November Run on:

US-10-797-893-8 2472 Title: Perfect score:

1 MGRCRLSKIGATRRPPPARV.....LEAKMLAQKAEEKENHCPTM Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

length: 0 length: 2000000000 seq Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

kinesin-related pr F25116.11 protein kinesin-like prote kinesin-like prote kinesin-lelated pr kinesin-related pr kinesin limported] kinesin family pro probable kinesin-l kinesin-like DNA b kinesin-like prote Description SUMMARIES S62328 T48258 A55236 A86319 IS1617 T18277 A56514 A47525 A67107 A633939 D86151 A54803 T30335 T02017 B84687 A48669 S38982 T14156 T48959 T51930 T10164 JC5831 T51932 E84792 % Query Match Length D Result Š

kinesin-related pr	kinesin-like spind	kinesin heavy chai	kinesin-related pr	kinesin-like prote	kinesin-related pr	kinesin heavy chai	kinesin-like prote	kinesin heavy chai	hypothetical prote	kinesin-related pr	kinesin-like prote	centromere protein	kinesin-like prote	kinesin heavy chai	hypothetical prote
S58691	G02157	S44868	A40264	A55289	S64238	A38713	833417	A35075	T20621	JN0114	T15822	S28261	T46242	837711	T06065
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742	1056	843	1060	1150	805	1031	1067	196	928	1584	1584	2663	813	1027	1121
21.6	21.5	21.4	21.3	21.2	21.1	21.1	21.1	21.0	21.0	21.0	21.0	20.9	20.9	20.7	20.7
533	532	529.5	525.5	525	522.5	520.5	520.5	519	518.5	518	518	517	516	512	511
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 S62328
kinesin-like DNA binding protein KID - human
C;Species: Homo sapiens (man)
C,Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
C;Accession: S62328
R; Tokai, N.; Fujimoto-Nishiyama, A.; Toyoshima, Y.; Yonemura, S.; Tsukita, S.; Inoue.
EMBO J. 15, 457-467, 1996
A, Title: Kid, a novel kinesin-like DNA binding protein, is localized to chromosomes an
A; Reference number: S62328; MUID: 96174806; PMID: 8599929
A; Accession: S62328
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-665 < TOK>
C; Superfamily: kinesin motor domain homology
C; Keywords: ATP; nucleotide binding; P-loop
F;44-374/Domain: kinesin motor domain homology <kmot></kmot>
F;128-135/Region: nucleotide-binding motif A (P-loop)

4 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAS-VLAYGPTGACKTHTMLGSPEQP 120 180 240 360 204 300 264 384 61 145 WGDPAGSHGPPAAHKGGGCRGPAMGLSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALG LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALG GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET GVI PRALMDILLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDILDPASGDLVIREDCRGN QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR Gaps 42; Score 2014; DB 2; Length 665; Pred. No. 1e-128; 3; Mismatches 44; Indels 4 Query Match
Best Local Similarity 82.4%;
Matches 416; Conservative ~ 62 98 121 205 265 325 181 241 301 a a 셤 g 8 8 ઠે ઠે ò 셤 8 ઠે 셤

KLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIER 460

401

361

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PVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAA-----------PASASQ 400

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C)Accession: A55236; E41298

R) Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.

J. Cell Biol. 127; 1441-1048, 1994

A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible ro
A;Reference number: A55236; MUID:95050960; PMID:7525600

A;Reference number: A55236

A;Reference number: A55236

A;Residues: 1-784 <-PES.
A;Residues: 1-784 <-PES.
A;Residues: L-784 <-PES.
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F;0-350/Domain: kinesin motor domain homology KMOI>
F;106-113/Region: mucleotide-binding motif A (P-loop)
F;350-S80/Domain: helical rod #status predicted KROD>
F;81-784/Domain: tail globular #status predicted KGD>
F;81-784/Domain: tail globular #status predicted KGD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYGSRAKSIQNQPIKNE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 TRRP------PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN
                           C;Species: Drosophila melanogaster
C;Species: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RGPEEEEI----
                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 'TC',222-337,'VRGQV' <STE>
A;Cross-references: GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 APLLSTPKRERMVLMKTVEEKDLBIER-----LKTKOKELEAKMLAQKAEE 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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24.8%; Score 612; DB 1; L
Best Local Similarity 33.0%; Pred. No. 1.4e-33;
Matches 175; Conservative 84; Mismatches 184;
N,Alternate names: kinesin-like protein 5; KLP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: FlyBase:Klp68D, KLP5
A;Cross-references: FlyBase:FBgn0004381
C;Function:
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                                                                                                                                                                                                                                                      kinesin-like protein - Arabidopsis thaliana
NiAlternate names: protein TIE22.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T4828
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24489
A;Reference number: Z24489
A;Reference number: Z24489
A;Reference number: Z24489
A;Residues: 1-664 <BEV>
A;Residues: 1-664 <BEV>
A;Residues: 1-664 <BEV>
A;Residues: 1-664 <BEV>
A;Residues: 1-664 <BEV>
A;Reperamental source: cultivar Columbia; BAC clone TIE22
C;Genetics:
A;Map position: 5
A;Mat position: 5
A;Mote: TIE22.130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAKLOAWLESKGKMKSAHRWMAIRSPLMGTNQTSISQSSVKKLLCHRSAIAESAKLAGTG 478
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                                   484
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        ---PGBPGAPLLSTPKRERMVLMKTVEEKDLEIER
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kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)
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32.1%; Pred. No. 8.2e-34;
tive 94; Mismatches 187; Indels
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Best Local Similarity
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C;Accession: I51617; A48835; S48837
R;Vernos, I.; Raats, J.; Hirano, T.; Heasman, J.; Karsenti, E.; Wylie, C.
Cell 81, 117-127, 1995
A;Title: XKLP1, a chromosomal Xenopus kinesin-like protein essential for spindle organ;
A;Accession: I51617
A;Reference number: A5621; MUID:95236444; PMID:7720067
A;Accession: I51617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1256 <VER>
A;Molecule type: mRNA
A;Residues: 1-126 <VER>
A;Cross-references: UNIPROT:091784; EMBL:X82012; NID:9562792; PIDN:CAA57539.1; PID:9567
B;Vernos, I.; Heasman, J.; Wylie, C.
Dev. Biol. 157, 232-239, 1993
A;Title: Multiple kinesin-like transcripts in Xenopus occytes.
A;Reference number: A48835
A;Title: Multiple kinesin-like transcripts in Xenopus occytes.
A;Reference number: A48835
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 9-162, 'L', 146-338 <VEZ>
A;Residues: 9-162, 'L', 146-338 <VEZ>
A;Residues: 9-162, 'L', 146-338 <VEZ>
A;Residues: 9-162, 'L', 146-338 <VEZ>
A;Residues: 9-162, 'L', 164-338 <VEZ>
A;Residu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 RLKLQVQEL--QVLLLQAHGGTLPVLNSMEPSENLQSLMERNKNLEKENG------ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 KLSRELGEAAVQTAQFL-----EKIIMTEQQNEK-----LGSKMEELKQHAACKVNLQR 450
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VRVALRCRPLVP------KENNEGCKWCLTFVPGEQQVIVGTEKSFTYDYVFDPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDLLQLTREEGAEGRP-WALSVTMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
23.4%; Score 579.5; DB 2; Length
Best Local Similarity 32.1%; Pred. No. 4.3e-31;
Matches 157; Conservative 95; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: klpl
C;Superfamily: kinesin motor domain homology
C;Superda: ATP; nucleotide binding; P-loop
F;9-43/Domain: kinesin motor domain homology «KMOT
F;87-94/Region: nucleotide-binding motif A (P-loop)
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RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Accession: A86119

RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Reizzo, M.; Roney, T.; Rowley, D.; Sakano, H. Li, Suuthwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86119

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-703 <STO>
A;Cross-references: UNIPROT:Q9FZ77; GB:AE005172; NID:g9795601; PIDN:AAF98419.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV-INRPFTNESLQPHALGPVKLSQ 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||| ::::||||||| : : :| : || : || || : || : || SLGGSCNTVMIANISPSSQSFGETQNTLHWADRAKEIRVKECEVNEEV-----VQVGE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                  F25116.11 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kineain-like protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| | :| | : | | : | | EBE--GADQAKILIJELQKE---NSELRVQLAKQQQKILITLQAENIAAANNNNNISLTPPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.2%; Score 597.5; DB 2; Length 33.9%; Pred. No. 1.2e-32; ive 88; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLK--
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Matches 173; Conservative
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A;Map position: 3
A;Introns: 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; 5
A;Note: F1612.60
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinesin-related protein-like - Arabidopsis thaliana
NiAlternate names: protein F1612.60
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Ciste: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
Cistes: 20-Apr-2000 #sequence_revision No. Apr-2000 #text_change 09-Jul-2004
Rijordan, N. is Bangertt, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, abubmitted to the Protein Sequence Database, March 2000
A; Reference number: 224468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 THTMLGS------PEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQ 119
                                                                                                                                                                                                        PGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA---SGDLVIRED 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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--- SDPPCVRGMDSCSLEIANWRNHQETLKYQF
                                                                                                                                                                                                                                                                                                                                                                           237 APFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR---
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29.5%; Pred. No. 3.4e-30;
tive 99; Mismatches 201; Indels
                                                       A;Residues: i-1058 < JOR>
A;Cross-references: UNIPROF:Q9LZU5; EMBL:AL162459
A;Experimental source: cultivar Columbia; BAC clone F16L2
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            PARVRVAVRLRPFV - - DGTAGA - - -
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Best Local Similarity 29.59
Matches 156; Conservative
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A; Molecule type: DNA
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A,Residues: 1-1225 <WAN>
A,Cross-references: UNIPROT:090640; GB:U18309; NID:g603760; PIDN:AACS9666.1; PID:g603761
R;Wang, S.Z.; Adler, R.
Proc. Natl. Acad. CST. U.S.A. 91, 1351-1355, 1994
A,Title: A developmentally regulated basic-leucine zipper-like gene and its expression i
A,Reference number: A53451; MUID:94151328; PMID:8108415
        Nicesession: 1.1. McCaffrey, G.; Vale, R.D.

Submitted to the EMBL Data Library, November 1995

A) Reference number: Z18853

A) Accession: T18277

A) Status: preliminary; translated from GB/EMBL/DDBJ

A) Molecule type: mRNA

A) Residues: 1-1254

A) Status: DESS CONTROL O94463; EMBL:U41289; NID:g1526990; PID:g1526991; PIDN:AABO77
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(S.Gyperfamily: unassigned kinesin-related proteins; kinesin motor domain homology
C,Keywords: ATP; DNA binding; mitosis; nucleotide binding; P-loop
P;11-344/Domain: kinesin motor domain homology <KMOT>
F,88-95/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: mRNA
A;Residues: 728-1086. RI' <WA2>
A;Cross-references: EMBL:U04821; NID:G440792; PIDN:AAA18960.1; PID:G440793
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22.9%; Score 567; DB 2; Length 12
Best Local Similarity 36.1%; Pred. No. 3.1e-30;
Matches 126; Conservative 79; Mismatches 132; Indels
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Accession: T18277
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ext_change 09-Jul-2004 angaku, M.; Hirokawa, N. stem. 303 G120469; PIDN:BAA02166.1; PID:g2204 G118911) G1F3A/3B heterodimer associates with Orovides anterograde fast axonal tra motor domain homology ner; microtubule binding; nucleotide	RESULT 10 A57107 Kinesin-related protein KIF3B - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 R;Vamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N. J. Cell Biol. 130, 1387-1399, 1995 A;Title: KIF3A,B: a heterodimeric kinesin superfamily protein that works as a microtubn A;Nolecule type: mRNA A;Reference number: A57107; MUID:96032268; PMID:7559760 A;Status: nucleic acid sequence not shown A;Nolecule type: mRNA A;Residues: 1-747 xxxxx A;Residues: 1-747 xxxx
Query Match         22.8%; Score 563.5; DB 1; Length 701;           Best Local Similarity 30.2%; Pred. No. 2.3e-30;           Matches 169; Conservative 83; Mismatches 184; Indels 123; Gaps 16;           QY         9 IGATRRPPPA-RVRVAVRLRPF	Query Match 22.8%; Score 563; DB 1; Length 747; Best Local Similarity 30.7%; Pred. No. 2.8e-30; Matches 169; Conservative 95; Mismatches 189; Indels 98; Gaps 16; Qy 20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKYQPDAFYGERST 75                              Db 10 VRVVVRCRP-MNGKEKAASYDKVVDVDVKLGQVSVKNPKGTSHEMPKTFTFDAVYDWNAK 68
QY         45 MDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGP 104           Db         59KTFTFDTVFGPESKQLDVYNLTARPIIDSVLEGYNGTIFAYGQ 101           QY         105 TGAGKTHTMLGSPEQPGVIPRALMDLL-QLTREEGAEGRPWALSVTMSYLEIYQEKV 160           I	Qy 76 QQDIYAGSVQPILRHILEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLL- 131    ::   ::   ::
OY 161 LDLL-DPASGDLVIREDCRGNILIPGLSGKPISSFADFERHFLPASRNRTVGATRLNQRS 219	Cy 191 ISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYL 248

Db 234 AAAQKPGAKKDDSNHVRVGKLNLVDLAGSERQDKTGATGDRLKEGIKINLSLTALGUVIS 293  286 ALNOGLP-RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNPAARSKEW 344	PRESULT 12  Highly  Probable kinesin-related cytokinesis protein [imported] - Arabidopsis thaliana C;Species Arabidopsis thaliana (mouse-ar cress) C;Species Arabidopsis thaliana (mouse-ar cress) C;Species Arabidopsis thaliana (mouse-ar cress) C;Species Arabidopsis thaliana (mouse-ar cress) C;Species Arabidopsis thaliana C;Space 02-b2001 R;Bin, X.; Raul, S.; Rounsley, S.D.; Shas, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salaberg, S.L.; Fraser, C.M.; Venter, Nattle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Stetus: prelaminary A;Accession: H84777 A;Stetus: prelaminary A;Rocession: H84777 A;Cocession: H84777 A;Co	OY 173 IREDCRGNILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
	nonas reinhardtii rdtii evision 07-Oct-1994 #text_change 09-Jul-2004 Hall, J.L.  d gene encodes a novel kinesin-homologous protein.  D:94299638; PMID:8027176  codon AAC for residue 753 as Asp  in-related proteins; kinesin motor domain homology ucleotide binding; P-loop domain homology *KWOT> ding motif A (P-loop)  ; Score 561.5; DB 2; Length 786;  pred. No. 3.8e-30;  RB; Mismatches 190; Indels 111; Gaps 19;  PFVDGTAGASDPPCVRGMDSCSLEIANWR-NHQETLK- 63  FLNGKEKADGRSRIVDMDVAGQVKVRNPKADASEPPKA 57  AGSVQPILRHLLEGONASVLAYGPPGAGKTHTMLGSPEOP 120	Db 58 FTPDQVPWNCQQRDVFDITARFLIDSCIEGYNGTIFAYGQTGTGKSHTMEGKDEPPELR 117  Qy 121 GVIPRALMDLLQ-LTREEGAEGREWALSVTWSYLEIYQEKVLDLL-DPASGDLVIREDCR 178

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P22M8.8 protein - Arabidopsis thaliana (mouse-ear cress)
(5)Species: Arabidopsis thaliana (mouse-ear cress)
(5)Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
(5)Accession: D86151
(5) Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 EEIVKSGKLNLVDLAGSENISRSGAREGRAREAGEINKSLLTLGRVINALVEHSGHIPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 ESKLTRLLRDSLGGKTKTCVIATVSPSVHCLEETLSTLDYAHRAKHIKNKPEVNQKMMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIA---NWRNHQETLKYQFDAFYGERSTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 NILIPGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 RQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMD---PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 MLERLLSLDRLLASQGSQGA---------PLLSTPKRERMVLMKTVEEKDL
                                                                                                                                                                                                                                                                                                                                                                A,Map position: 2
C,Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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22.7%; Score 560.5; DB 2
Best Local Similarity 31.0%; Pred. No. 6.9e-30;
Matches 159; Conservative 94; Mismatches 199
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                        RESULT 14
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                                                                                                                                                                                                                                                                                   C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T02017
R;Asada, T.; Kuriyama, R.; Shibaoka, H.
J. Cell Sci. 110, 179-189, 1997
A;Title: TKRP125, a Kinesin-related protein involved in the centrosome-independent organ
A;Reference number: 214490; MUID:97196959; PMID:9044048
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1006 <ASA>
A;Residues: UNIPROF:023826; EMBL:D83711; NID:g2582970; PIDN:BAA23159.1; PID:g258
                                                                         459
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RPFTNESLQPHALGPVKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQ 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 LVEHLGHIPYRDSKLTRLLRDSLGGRTKTCIIATVSPAVHCLEETLSTLDYAHRAKNIKN 357
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                                                                                                                                                                                                                                                                    Inesin-related protein TKRP125 - common tobacco
Species: Nicotiana tabacum (common tobacco)
Date: 26-Peb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
                                                                                             10 VQVLRCRPFSNDELRNNAPQVVTCNDYQREVAVSQNIAG--KHIDRI-FTFDKVFGPSA
                                                                     KLSSMDPAMLERLLSLDRLLASQGSQGAPLLSTPKR-----ERMVLMKTVEEKDLEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-------PBQPGV
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A;Residues: 1-1006 <ASA>
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C;Genetics:
A;Note: TKRP125
C;Superfamily: kinesin-related protein Eg5; kinesin motor domain homology
F;10-361/Domain: kinesin motor domain homology <KMOT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.7%; Score 560.5; DB 2; Best Local Similarity 30.1%; Pred. No. 6.3e-30; Matches 153; Conservative 98; Mismatches 196;
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                               KPEVNOKMMKSTL----IKDLYGE-
                                                                                                                                            RLKTKOKELEAKMLAOKAE 478
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Nature 408, 816-820, 2000

AjAuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.N.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Accession and analysis of chromsome lof the plant Arabidopsis.
A;Reference number: A86111
A;Reference number: A86111
A;Residues: Dramary
A;Residues: L-885 <STO>
A;Residues: L-885 <STO>
A;Residues: L-885 <STO>
C;Genetics:
A;Rap position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM--LG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 SPEQP--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 LSLSALGKCINAIAENSPHVPLRDSKLTRLLRDSFGGTARTSLIVTIGPSPRHRGETTST 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | : | | : | | : | 393 ILFGQRAMKVENMLKIKEEFDYKSLSKKLEVQLDKVIAENERQLKAFDDDVERINRQAQN 452
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89; Mismatches 203; Indels
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Search completed: November 5, 2004, 18:45:35 Job time: 16.1982 secs

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5, 2004, 18:34:16 ; Search time 297.595 Seconds (without alignments) 1813.185 Million cell updates/sec
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(c) 1993' - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                   protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 90071, A Sequence 90071, A Sequence 90072, A Sequence 90098, A Sequence 90098, A Sequence 90096, A Sequence 90096, A Sequence 90099, A Sequence 90099, A Sequence 90099, A Sequence 90099, A Sequence 1228, Ap Sequence 1228, Ap Sequence 1228, Ap Sequence 11424, A Sequence 11424, A Sequence 11425, A Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 149034, Sequence 10346, Sequence 537, Appli Sequence 547, Appli Sequence 54 Sequence 8784, Ap Sequence 90071, A Sequence 90071, A Sequence 4, Appli Sequence 425, App Sequence 10738, A Sequence 8784, Ap Sequence 80, Appl Sequence 80, Appl Sequence 80, Appl Sequence 7228 Sequence 1676 Sequence 5166 ASA Description Sequence Sequence PCT-US03-02234-80
US-10-949-016-8784
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LIGNMENT

RESULT 1
US-09-597-292-8
1 Sequence 8, Application US/09597292
2 Sequence 8. Application US/09597292
3 GENERAL INFORMATION:
3 APPLICANT: Beraud, Christophe
3 TITLE OF INVENTION: their use
4 FILE REFERENCE: 1044
5 CURRENT APPLICATION NUMBER: US/09/597,292
6 CURRENT PILING DATE: 2000-06-20
7 PRIOR APPLICATION NUMBER: US 09/295,612
7 PRIOR PILING DATE: 1999-04-20
7 WUMBER OF SEQ ID NOS: 8
7 SOFTWARE: FastSEQ for Windows Version 4.0
7 SEQ ID NO 8
7 LENGTH: 487
7 TYPE: PRT
7 TYPE: PRT
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                                                  181 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel motor proteins an TITLE OF INVENTION: Novel motor proteins an TITLE OF INVENTION: their use TITLE OF INVENTION: their use CURRENT APPLICATION NUMBER: US/09/597,292; CURRENT FILING DATE: 2000-06-20 PRIOR APPLICATION NUMBER: US 09/295,612 PRIOR PILING DATE: 1999-04-20 NUMBER OF SEQ ID NOS: 8
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FastSEQ for Windows Version 4.0
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ENHCPIM 487
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        Length 487;
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GENERAL INFORMATION:
TITLE OF INVENTION: Christophe
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR PILICATION NUMBER: US/99/724,224
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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     Query Match 100.0%; Score 2472; DB 19; Best Local Similarity 100.0%; Pred. No. 1.3e-204; Matches 487; Conservative 0; Mismatches 0;
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GENERAL INDORMATION:
GENERAL INDORMATION:
APPLICANT: Jean-Philippe Girard
APPLICANT: Francois Amalric
APPLICANT: Francois Amalric
APPLICANT: Francois Amalric
APPLICANT: Thomas Clouaire
APPLICANT: Thomas Clouaire
TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
TITLE OF INVENTION: TRAP PROTEINS AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
ITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
FILE REFERENCE: BIOBANK: 012A
CURRENT APPLICATION NUMBER: 05/10/733,878
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 66/485027
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 535
SOF ID NO 425
LENGTH: 665
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99.8%; Score 2467; DB 33;
Best Local Similarity 100.0%; Pred. No. 5.9e-204;
Matches 486; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-733-878-425
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US-10-733-878-425
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Sequence 4, Application US/10797893

GENERAL INPORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893

CURRENT APPLICATION NUMBER: US/09/724,224

PRIOR APPLICATION NUMBER: US/09/724,24

PRIOR APPLICATION NUMBER: US/09/724,24

PRIOR PILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/597,292

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 512

TYPE: PRI
CREANISM: Human
US-10-797-893-4
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NHCPTM 512
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Query Match
Best Local Similarity 100.0
Matches 455; Conservative
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; LENCTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-USO2-41687-80
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                                                                                                    APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPRESENCE: CLOOL331
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SQOTPMARE: Patentin version 3.2
SQOTPMARE: Patentin version 3.2
SEQ ID NO 10738
LENGTH: 482
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GENERAL INFORMATION:
APPLICANT: SUGEN, INC.
APPLICANT: SUGEN, INC.
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REPERENCE: 038602/1544
CURRENT APPLICATION NUMBER: PCT/US02/41687
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/43,169
PRIOR APPLICATION NUMBER: 60/43,169
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATCHING DATE: 201-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATCHING DATE: 201-12-31
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93.4%; Score 2309; DB 27;
Best Local Similarity 100.0%; Pred. No. 1.8e-190;
Matches 455; Conservative 0; Mismatches 0;
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                                                                             Sequence 10738, Application US/10170205E
GENERAL INFORMATION:
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US-10-170-205E-10738
         506 NHCPTM 511
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Sequence 80, Application PC/TUS0302234

GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR V.
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASE IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1571
CURRENT APPLICATION NUMBER: PCT/US03/02234
CURRENT FILING DATE: 2003-01-28
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
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93.4%; Score 2309; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.8e-190;
Matches 455; Conservative 0; Mismatches 0;
     Score 2309; DB 1; L
Pred. No. 1.8e-190;
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93.4%; Sco. 100.0%; Pred. No. ...
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TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLOPHALGP 361
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Sequence 80, Application US/10334143

GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: MITCHED WITH THE METHOD
FILE REPERENCE: 038602/1543
CURRENT APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR APPLICATION NUMBER: 2001-12-31
SEQ ID NOS: 207
SOFTWARE: PALENTIN Ver. 2.1
                                                                                      394 VKLSQKELLGPPEAKRARGPEEEEIGSPEPWAAPASASQKLSPLQKLSSMDPAMLERLLS
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                                                                                                                                 LDRILASQGSQGAPLLSTPKRBRNVLMKTVEEKDL 456
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ORGANISM: Homo sapiens
US-10-334-143-80
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GENERAL INFORMATION:
APPLICANT: VOTTER, J. Craig et al.
TILE OF INVENTION: DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
SEQ ID NOS: 207012
SEQ ID NOS: 207012
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, ORGANISM: Homo sapiens US-09-724-676-90071
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              SEGUREAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/10/940,774

CURRENT FILING DATE: 2004-03-15

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 8784
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| GENERAL INFORMATION:
| APPLICANT: Compagen LTD:
| TILLS OF INVENTION: Variants of alternative splicing
| TILLS OF INVENTION: Variants of alternative splicing
| FILE REFERENCE: 129181.4 Compagen
| CURRENT APPLICATION NUMBER: US/09/724,676
| CURRENT FILING DATE: 2000-11-28
| NUMBER OF SEQ ID NOS: 97222
| SEQ ID NO 90071
| LENGTH: 559
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     Seguence 8784, Application US/10940774
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US-09-724-676-90071
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US-10-940-774-8784
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US-09-724-676A-90071
IS-09-724-676A-90071
Sequence 90071, Application US/09724676A
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants US/09/724,676A
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: DEMONTORY
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90.4%; Score 2235; DB 21;
Best Local Similarity 99.8%; Pred. No. 5.9e-184;
Matches 442; Conservative 1; Mismatches 0;
Score 2235; DB 21;
Pred. No. 5.9e-184;
1; Mismatches 0;
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CORGANISM: Homo sapiens
US-09-724-676A-90071
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US-09-724-676-90072

Sequence 90072, Application US/09724676

GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 90072
LENGTH: 588
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Best Local Similarity 99.8
Matches 442; Conservative
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US-09-724-676-90072
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Sequence 90072, Application US/09724676A; GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TITLE OF INVENTION: Variants of alternative spl:
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A;
CURRENT APPLICATION NUMBER: US/09/724,676A;
NUMBER OF FILING DATE: 2000-11-28;
NUMBER OF SEQ ID NOS: 97222;
SOFTWARE: PatentIn version 3.2;
SEQ ID NO 90072;
LEMOTER: FAS
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Search completed: November Job time : 299.595 secs

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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate aspents that are capable of modulating the activity of target proteins having motor of modulating the activity of target proteins having motor or phosphate. Purthermore, this activity or indirectly produces ADP fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; concer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human kinesin-like DNA binding protein (KID) (SeqID 8).
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AAU79590
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20-JUN-2000; 2000US-00597292.
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N-PSDB; ADC23343.
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              GenCore (c) 1993
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                                                                                                                                             MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE
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                                                                                                                       Gaps
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                                                                                               Score 2472; DB 7;
Pred. No. 6e-224;
0; Mismatches 0;
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Best Local Similarity
                                                                          Sequence 487 AA;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restences, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular confileration disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and for inhibiting CC associated with KID and contain motor protein cC and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and 
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ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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Best Local Similarity 100.
Matches 487; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP for phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 4) of the invention.
SLDRLLASOGSOGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEK 480
                                                                                                                                                                                                                                        human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostetic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate agent as modulator of function of a targ
protein for treating cellular proliferation disorders by adding
candidate agent to a mixture of the target protein that
directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.8%; Score 2467; DB 7; Length 512; 100.0%; Pred. No. 1.9e-223; Ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                            Human kinesin-like DNA binding protein (KID) (SeqID 4).
                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by CA"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4; 26pp; English
                                                                                                                          ADC23340 standard; protein; 512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2000; 2000US-00724224
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CYTO-) CYTOKINETICS INC.
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                                             ENHCPTM 4
                           ENHCPTM
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                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                 US6387644-B1.
                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                       ADC23340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beraud C;
421
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ADC23340
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Human; microtubule motor protein; cellular proliferation disorder; cardiac hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
Human microtubule motor protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00295612.
2000US-00597292.
2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CYTO-) CYTOKINETICS INC.
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Best Local Similarity 100. Matches 486; Conservative

2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 

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Gaps

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or concert, hyperplasias, restenosis, cardiac hypertrophy, immune disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders screening for modulators of motor proteins useful for treating cellular confidention for modulators of motor proteins useful for treating cellular confidention disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and diseases, arthritis, graft rejection, inflammatory bowel disease and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is concern by the nucleic acid featured as SEQ ID NO:3, but this does not Claim 1; SEQ ID NO 4; 26pp; English appear to be the case. &\$38888888888888888888888888888888

Sequence 512 AA;

146 206 241 266 301 361 TRILIQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP 386 421 LDRLLASQGSQGAPLLSTPKRERMVLMKTVBEKDLEIERLKTKQKELEAKMLAQKAEEKE 481 121 181 86 362. VKLSOKELLGPPEAKRARGPEEEEIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLS 62 LKYQFDAFYGERSTQQDIYAGSYQPILRHLLEGQNASYLAYGPTGAGKTHTMLGSPEQPG VIPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNI LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL TRILLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP 387 VKLSÇKELLGPPEAKRARGPEEETGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS 2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET Gaps .; 0 Length 512; Indels 99.8%; Score 2467; DB 8; L 100.0%; Pred. No. 1.9e-223; 100.0%; Prec. ... Best Local Similarity 100. Matches 486; Conservative NHCPTM 487 Query Match Best Local Similarity 207 242 267 327 482 507 122 302 182 셤 g 셤 셤 ò 셤 à ò 원 g ò ઠે 셤 ò à ò

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Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                            thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; appbrosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; encroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                                                                                                                                                                                                                    Clouaire T;
                                                                                                                                                                                                                     Roussigne M,
             protein SEQ ID NO:425.
                                                                                                                                                                                            ENDOCUBE SAS.
CNRS CENT NAT RECH SCI.
                                                                                                                                                                 10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P.
                                                                                                                                                10-DEC-2003; 2003WO-IB006434.
                                                                                                                                                                                                                      Girard J, Amalric F,
                                                                                                                                                                                                                                       WPI; 2004-525034/50.
                                                                                                                                                                                                                                                 N-PSDB; ADQ09241
                                                                                                               WO2004055050-A2
                                                                                              Homo sapiens.
                                                                                                                                01-JUL-2004.
23-SEP-2004
                Human KNSL4
                                                                                                                                                                                            (ENDO-) 1
(CNRS ) (
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Example 47; SEQ ID NO 425; 612pp; English.

The present invention describes a method for modulating the expression of a thanacos (death)-associated protein (THAP) responsive gene. The method completes modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP responsive complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy consisting a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family of DIYPeptide or its bloidgical fragment, or a nucleic acid and a THAP-family polypeptide or its bloidgical fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (6) a vector packaging cell line comprising a viral vector which comprises a promoter operably linke conclusion of constructing a cell which expresses creament; (7) a method of constructing a cell which expresses creament; (7) a method of constructing a cell which expresses creament; (7) a method of constructing a cell which expresses creament; (7) a method of constructing a cell which expresses creament; (8) are those of identifying a test compound that modulates transcription a creament or that modulates the transport of a THAP-family polypeptide from accessive or insufficient approsis, cardiovascular disease and neurodegenerative corpusing a test compound that modulates transcription associated with a condition associated with a c

ADQ09240 standard; protein; 665 AA. ADQ09240; RESULT 5 ADQ09240

Homo sapiens.

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cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                  GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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                                                                                                                                                                 Length 665;
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                                                                                                                                                              99.8%; Score 2467; DB 8; L
100.0%; Pred. No. 2.9e-223;
1ve 0; Mismatches 0;
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                                                                                                                                                                              Local Similarity
                                                                                        diseases. The prespreser
                                                                                                                                   Sequence 665 AA;
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The invention elates to novel isolated, enriched or purified mucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and condoss a naturally occurring kinase polypeptide; (d) encodes the conformal domain, a cerept that it lacks one or more, but not all, of an CV terminal domain, a coiled-coil structure region, a spacer region and a CV terminal domain, a coiled-coil structure region, a spacer region and a CV terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or curronal-associated diseases, and metabolic disorders. The disorders are CV preferably cancers of the tissues or of hemacopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, corrections caused by fungi, ocular disease, migraines, pain, bacteria, infections caused by fungi, ocular diseases, migraines, pain, coviral infections caused by fungi, ocular diseases, migraines, pain, coviral infections in whypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant corresponds to one of the kinase polypeptides of the criefficion. This sequence corresponds to one of the kinase polypeptides of
                                                                                                                                                                                                                                                                                                                                                                New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 80; 491pp; English.
                                                                                                                             31-DEC-2002; 2002WO-US041687
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                                                                                                                                                                                                                                                                                Grigoriev IV, Sudarsanam
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                                                                                                                                                                                                                                                                                                                                                                                                                               metabolic disorders.
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                                          WO2003057841-A2.
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242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
                                                                                                                                                                                                                                                                                                                                                                               VKLSQKELLGPPEAKRARGPEEEEIGSPEPWAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                             LIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFRO
                                                                                                                                                                                                                                                     TRILIQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                            LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                            VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                               4 GRCRLSKIGATRRPPFARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                           GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQET
Mismatches
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20-JUN-2000; 2000US-00597292.
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   Conservative
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   422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC23342;
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilifective; gynaecological; antibacterial; gone therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                        421
                                                                                                        453
      TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP 361
                                                                                          VKLSQKELLGPPEAKRARGPEEEBIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer antigen protein sequence SEQ ID NO:1228.
                                                                                                                                                              LDRILLASQGSQGAPLLSTPKRERMVLMKTVEBKDL 456
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                                                                                                                                                                                                                                                                AAB56650 standard; protein; 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US005988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270P
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens, useful for tre
such as prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
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N-PSDB; AAF15853.
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21-SEP-2000

Ношо

13-MAR-2001

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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
Human kinesin-like DNA binding protein (KID) (SeqID 6)
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Length 460;

Score 2141; DB 3; Pred. No. 9.6e-193;

86.6%;

Query Match Best Local Similarity Sequence 460 AA;

invention

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ADC23338 standard; protein; 370
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Best Local Simi
Matches 346;
                                       Beraud C;
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                     This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces to phosphate. Furthermore, this activity can be determined using method fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a farmonomodulators and antinflammatories. Accordingly, through gene thermappy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                   GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGN 180
                                                                                                                                                                                                                                                                                                                                                                               QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                                                                                                                                                                                                 TLKYOFDAFYGERSTQODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP
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0; Indels
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Claim 1; SEQ ID NO 6; 26pp; English.
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28-NOV-2000; 2000US-00724224.
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Best Local Similarity 100.
Matches 346; Conservative
                                                                                                                                                                                              Sequence 346 AA;
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cacids encoding them. The invention also relates to a method of screening acids encoding them. The invention which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, method of catidity candidate agents that bind to a target protein, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for proliferation disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune disorders and inflammation, for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and anglophasty. This sequence represents a human microtubule motor protein
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                                                                                                                                                                                                                                                                          New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
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100.0%; Pred. No. 1e-157;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 6; 26pp; English.
(CYTO-) CYTOKINETICS INC.
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                                                                                                                                                   WPI; 2004-532491/51
N-PSDB; ADQ60231.
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                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
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REGKLYLI DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL

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Human kinesin-like DNA binding protein (KID) (SeqID 2).
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                                                                                          20-APR-1999; 99US-00295612
20-JUN-2000; 2000US-00597292
                                                                                 28-NOV-2000; 2000US-00724224
                                                                                                        (CYTO-) CYTOKINETICS INC
                                                                                                                          WPI; 2003-706919/67.
                                                                                                                               N-PSDB; ADC2337.
                                                  Misc-difference 1
                                                                                                                                                                                                                                        Sequence 370 AA;
                                                                US6387644-B1
                                     Homo sapiens
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cor modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA correction of sorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders of motor proteins useful for treating cellular corrections of sorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and corrections and protein surgery and candioplasty. This sequence represents a human microtubule motor protein cof the invention. Note: The specification states that this sequence is concerned by the nucleic acid featured as SEQ ID NO:1, but this does not
Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                   TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                           Human microtubule motor protein #1.
                                                                                                                                                                                                                                                 ADQ60228 standard; protein; 370
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-532491/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using or phosphate. Furthermore readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antinfinammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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                                                  human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                                                                                                                     /note= "Encoded by ATGCA"
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Best Local Similarity Matches 345; Conserr

Query Match

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408 LQVSTIEQPVEDDSDPE---GAESESDKENEAEVAKSNEELERERVEN-SKLAAKLAELE 463
                                                                                                                                                                     :||| : || || || : || || || 5 SRRPGIGSSQTPNECVVRVRRCRPMSURERSERSPEVVNVYPNRGV----VELQNVVDGN
                                                                                                                                                                                                       58 HQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L
                                                                                                                                                                                                                                                                                                                                      DPQ-----DAKLKEYQESIERLKRLIGPQQQQRSEKQVTAKKQRVKKPKKETVTKEMSDS
           ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                  TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLBIANW--RN
                                                                                                                                                                                                                                                              GSPEQPGVI PRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
                                                                                                                                                                                                                                                                                                                    REDCRGN-ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQ
                                                                                                                                                                                                                                                                                                                                                                          233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP
                                                                                                                                                                                                                                                                                                                                                                                            : ||| |||||||| :|| CD-TETNTIKVGKLNLIDLAGSERQSKTGASAERLKEASKINLALSSLGNVISALAESSP
                                                                                                                                                                                                                                                                                                                                                                                                                               293 RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYASRAKSIONOPIKNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                              Length 784;
                                                                                             ; Score 616; DB 4; Length 78;
; Pred. No. 2.1e-48;
84; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 22341
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2000US-00614150.
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                                                                                         Query Match
Best Local Similarity 33.14
Matches 176; Conservative
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                                                                  Sequence 784 AA;
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                                                                                                                                                                                                                                                                                     242 REGKLYLIDLAGSEDNRRTGNKGIRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 301
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                                                                                                                                       LKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQPG
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                                                               GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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            Length 370;
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                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 40128.
                         3.3e-157;
            DB 8;
                                      Mismatches
          Score 1763;
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71.3%; SCOL.
100.0%; Pre
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11-JUL-2000; 2000US-00614150.
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                      Similarity
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                         Local Simines 345;
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human kinase protein #33

Novel

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                             20 VRVAVRLRPFVDG--TAGASDPPCVRGMD-SCSLEIANWRNHQETLKYQFDAFYGERSTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 LVDLAGSERQSKTQASGQRLKEATKINLSLSVLGNVISALVDGKSTHIPYRNSKLTRLLQ
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                                                                                                                         Disclosure; SEQ ID NO 22341; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                      Length 677;
                                                                                                                                                                                                                                                                                                                                      24.0%; Score 593; DB 4; Length 67 33.9%; Pred. No. 2.5e-46; ive 78; Mismatches 190; Indels
Myers EW;
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  PWD,
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GGENLLEKAQTQE 486
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Best Local Similarity 33.9%
Matches 167; Conservative
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  Venter JC, Adams M,
                                            N-PSDB; ABL09286
                                                                                                                                                                                                                                                                                                                 Sequence 677 AA;
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                                                                                    genes from Dr
interactions.
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a naturally occurring kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and condess a naturally occurring kinase polypeptide; (d) encodes the conditions to (a) and conjugatide; (d) encodes the conditions to (a) and conjugatide; (d) encodes the conditions of the cerminal domain, c-terminal catalytic domain, a C. terminal tail; or (e) is a complement of (d). The nucleic acid molecules, terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases and metabolic disorders. The disorders are neuronal-associated diseases, and metabolic disorders are for eneuronal-associated diseases, and metabolic disorders and iseases of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's diseases, conditions or viral infections caused by Fiungi, ocular diseases, migraines, pain, carceria, infections caused by Fiungi, ocular diseases, migraines, pain, diseases, dispendents, infections caused by Fungi, ocular diseases, migraines, pain, disorders, dyskinesias, metabolic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant crejections rejections crejections or of the kinase polypeptides of the rejections or or the kinase polypeptides of the rejections or or the conference of the kinase polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated, enriched or purified nucleic acid molecule encoding a
kinase polypeptide, useful for treating cancer, immune-related diseases,
cardiovascular disease, brain or neuronal-associated diseases and
                             cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; neurological disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-2001; 2001US-0343169P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      31-DEC-2002; 2002WO-US041687
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Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                               WO2003057841-A2
                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide (a) comprising any the 666 fully defined nucleotide sequences appearing as ADD49269 - ADD49935, ADD49356 and ADD49938, complements of (a); sequences of at least 20 contiguous residues of (a); sequences that hybridise to (a) under highly stringent conditions; sequences having at least 75 or 90% identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide ((b) (comprising: sequences encoded by the new
                                                                                                         IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGN
           AELNHLKQ------QVQQLQVLLLQAHGGTLPGSINAEPSEN----LQSLMEKNQSLVEE
                                                                                                                                                                                                                                             LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKQK-ELEAKMLAQK
                                                                                                                                                                                                                                                           ILIPGLSOKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDORERLAPFR
                                                                                             OREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVIGKVVDALNQGLPR--VPYRD
                                                                                                                                              SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA
                                                                                                                                                                                            LGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; cytostatic; lung cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lung specific tumour antigen L 1447p.
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                                                                                                                                                                                                                                                                                                                                                                               ADD49938 standard; protein; 1232 AA.
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vaccine; T-cell; tumour
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N-PSDB; ADD49936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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polymucleotide, any of the 4 amino acid sequences fully defined in the sequence in (a) or (b)), an expression vector comprising the above capteration (a) or sequence having at least 70 or 904 identity to the sequence in (a) or sequence having at least 70 or 904 identity to the sequence in (a) or (b)), an expression vector comprising the above polymucleotide operably linked to an expression control sequence, a not isolated antibody, or its antigent below expression vector, and isolated antibody, or its antigent by the polyment conditions, a chuston protein comprising a no oligonucleotide that hybridises to the parsence of a cancer in a patient (comprising) obtaining a biological sample from the patient; contacting the biological sample with a binding apent, or an amount of a polymelectide that binds to the binding apent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide that binds to the binding agent, or an amount of a polymelectide, to a predetermined cut-off value and than decembining the presence of a cancer in the polymucleotide, and than decembining the presence of a cancer in the oplymucleotide, buds conditions and/or arganding or antigen-presenting cells that expansion of the similation and/or expansion of T-cells with the above composition and a second tomponent selected from the above composition and antigen-presenting cells that express the above composition and antigen-presenting cells that express the above composition and antigen-presenting cells that express the above composition and antigen-presenting cells that express the above composition and antigen present on a patient the above and a decection reagent comprises a reporter group). The composition and effection reagent comprises a reporter g 109 165 225 293 286 VPYRDSKLTRLLQDSLGGNSHTLMIACVSPADSNLEETLNTLRYADRARKIKNKPIVNID 345 PQTABLINHLKQQVQQLQVL----LLQAHGG------TLPGSITVEPSENLQSLME 390 353 49 DCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRER 20 VRVAVRLRP-------FVDGTAGASDPPCVRGMDSCSLEIANWRNHQETLKY VRVALRCRPLVPKEISEGCOMCLSFVPG----EPQVVVGTDK-----SF 65 QFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS----PEQ P--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPA--SGDLVIRE LAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--226 SDKNSSFRSKLHLVDLAGSERQKKTKAEGDRLKEGININRGLLCLGNVISALGDDKKGGF VPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNES LQPHALGPVK--LSQKELLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSP-LQXLSS MDPAMLERLISLDRILASQGSQGAPLLSTPKRERMVIMKTVEEK-DLEIERLKTKQK-EL Gaps 75; Length 1232; 23.2%; Score 574.5; DB 7; Length 32.5%; Pred. No. 3.6e-44; ive 97; Mismatches 161; Indels Conservative Best Local Similarity Matches 160; Conserv Sequence 1232 AA; 10 120 110 236 354 Query Match Best Local & 20 176 166 346 셤 ઠે 셤 ò 셤 ò 유 ò g 요 ∙& ò

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391 KNQSLVEENEKLSRGLSEAAGQTAQML----ERIILTEQANEKMNAKLEELRQHAACKL 445 рp

469 EAKMLAQKAEEKE 481 : : | : | :: | 446 DLQKLVETLEDQE 458

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Search completed: November 5, 2004, 18:44:42 Job time : 101.956 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			181	74	112	54	901	72	53	58	99	69	66	83	77	908	191	960	64	15	81	38	197	36	20	92
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de	Query	Match	99.3	98.1	93.8	93.6	89.9	88.0	87.8	84.5	83.8	82.6	82.6	82.2	81.5	81.4	81.2	79.8	79.8	79.7	79.6	77.3	77.3	77.3	76.4	76.1
		Score	1107.4	1093.4	1045.4	1043.4	1002.8	980.8	978.6	942	934	921.4	921.4	917	606	907.8	908	889.8	9.688	889.2	887.4	862.4	861.8	961.6	851.8	848.8
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Query Match 99.3%; Score 1107.4; DB 3; Length 2057; Best Local Similarity 99.9%; Pred. No. 3.3e-294; Matches 1108; Conservative 0; Mismatches 1; Indels 0;

ORIGIN

BX399192 BW53107 BW653107 BW653107 BW6053671 BW6053671 BW6053671 BW6053671 BW341048 BW341048 BW341048 BW531647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW527647 BW60011 BW521359 BW66011 BW521359 BW66011 BW337059 BW521359 BW521359 BW521359 BW521359 BW521359 BW5681241 BW337059 BW343522 BW343522 BW343522 BW343522 BW343522 BW343522 BW343522 BW343522 BW343522 BW343529 BW35806 BW331772 BW35800 BW31772 BW35800 BW31772 BW35800 BW31772 BW35800 BW31772 BW35800 BW31772 BW36819	ALIGNMENTS 2057 bp mRNA linear HTC 21-JUL-2004 CSODK012YE23 of HeLa cells Cot 25-normalized).	Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo. Jessee, J. and Polayes, D. varies and normalization j Email : fliang@lifetech.com URL : vitrogen.com/ InVitroGen Corporation 1600	Genoscope - Centre National de Sequencage : c - FRANCE (E-mail : seqref@genoscope.cns.fr.ns.fr.ns.fr. and.th a NotI-oligo(dT) primer. Five primerand obNA was digested with Not I and cloned N v sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a	lfiers no sapiens" ha. 9666" 1127823" YSPORT_6"
844 75.7 990 5 B 836.4 75.0 1139 4 B 83.6 8 33.6 74.8 831 5 B 831.8 74.7 838 5 B 831.8 74.7 838 5 B 823 74.7 838 823 73.8 823 73.8 842 5 B 815.2 73.5 872 5 B 808.6 72.5 873 5 B 808.6 72.5 873 5 B 808.6 72.5 873 5 B 809.1 71.8 849 5 B 878 78.7 70.6 813 4 5 B 786.4 70.5 911 5 B 878.1 786.4 70.1 913 5 B 878.1 781.4 70.1 913 5 B	CR615781  ON full-length cDNA clone of Homo sapiens (human CR615781.  CR615781.  HTC; CNSLT_CDNA.  Homo sapiens (human)	Eukaryota; Metazoa; Mammalia; Eutheria; 1 (Basea 1 to 2057) Li, W.B., Gruber, C., Full-length CDNA lib Unpublished Contact: Feng Liang http://fulllength.in Faraday Avenue 2 (bases 1 to 2057)	S Genoscope.  Direct Submission  Submitted (20-JUL-2004) Genos  BP 191 91006 BVRY cedex - FRA  BP 191 91006 BVRY cedex - FRA  18t strand cBNRA was primed wi end enriched, double-strand cinco the Not I and EcoR V sit was normalized Library was c division of Invitroden.	
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RESULT 2
CR590974
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Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                    21-JUL-2004
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Catarrhini; Hominidae; Homo.
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| /organism="Homo sapiens" |
| /db_Xref="taxon:9606" |
| /clone="CSOD1009Y01" |
| /tissue type="Placenta Cot 25-normalized" |
| /plasmid="pCMVSPORT_6"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpull-length cDNA libraries and normalization
Unpublished
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98.1%; Score 1093.4; DB 3.
Best Local Similarity 99.9%; Pred. No. 2.4e-290;
Matches 1094; Conservative 0; Mismatches 1;
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FTC: CNSLT_CDNA.
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                                                                                                         VERSION
KEYWORDS
SOURCE
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref=taxon:9606"

/clone="CSODIOOYJO1"

/tissue type="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="lst strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was
digested with not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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   was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI009CE01QP1&c=7766.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1124;
                                                                                                                                                                                                                                                                                                                                     93.8%; Score 1045.4; DB 1; Length 96.6%; Pred. No. 3.8e-277; ive 24; Mismatches 11; Indels
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Matches 1059; Conservative
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BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library
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1 (Bases 1 to 1124)

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

15, W.B., Gruber, C., Jessee, J. and Polayes, D.

15, W.B., Gruber, C., Jessee, J. and normalization

15, Unpublished (2011)

16 on Feb 15, 2001 this sequence version replaced gi:31267547.
                    GATCCCGCGGGCCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGTGCCGAGGCCC
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
181 strand conscope.cns.fr)
182 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division Location/Qualifiers
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                                                                                                                                                                AAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCACAGCTCA 978
  TCATGCTGTGCTCCTGGTCAAGGKGGACCAGCGGRACGTTTGGCCCCATTTCGCCAGCG 780
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Homo sapiens
Homo sapiens
Homes, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, Was. (gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Mulbblished
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                                                AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAA
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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.larity 99.9%; Pred. No. 1.5e-276;
Conservative 0; Mismatches 1; Indels 0;
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/mol_type="mRNA"
/db_xref="txxon:9606"
/clone="CSODI040Y106"
/tissue_type="Placenta Cot 25
/plasmid="pCWVSPORT_6"
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CR590954.1 GI:50471761
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AUTHORS
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JOURNAL
REMARK
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AUTHORS
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Basea 1 to 1083)
1. (Basea 1 to 1083)
2. Li,W.B., Gruber.C., Jessee, J. and Polayes, D.

Rull-length cDNA libraries and normalization

1. (Dubblished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283903.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
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Homo sapiens
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Homo sapiens
Homo sapiens
Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1027)
Si Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30341614.
Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                               EST 07-APR-2004
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1027 bp mRNA linear EST 07-APR-200-
BX337406 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODIO41YII3 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Flist prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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89.9%; Score 1002.8; DB 5; Length 1027;
Best Local Similarity 99.5%; Pred. No. 2.1e-265;
Matches 1023; Conservative 3; Mismatches 0; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                   BX337406.2 GI:46274820
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Ist strand cDNA was primed.with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVgPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lit strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 2, 2003 this sequence version replaced Contact: Genoscope Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1032)
Li, W.B. Gruber, C., Jessee, J. and Polayes, D.
Lill-length cDNA libraries and normalization
Unpublished (2001)
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llarity 98.6%; Pred. No. 1e-258;
Conservative 4; Mismatches 8;
TTCGCCAGCGAGAGAAACTCTACCTGATTGACTTGGC
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|clone="CS0DI040Y106"
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Homo sapiens
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Best Local S
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                               1;
 Length 959;
                             0; Indels
 Score .942; DB 5; I
Pred. No. 1.3e-248;
0; Mismatches 0;
Query Match
Best Local Similarity 99.9%;
Matches 953; Conservative
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BX363358 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK012YE23 5-PRIME, mRNA sequence.

DEFINITION

BX363358.2 .GI:46287820 EST. Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE

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Gaps

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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqretégenoscope.cns.fr. Web : www.genoscope.cns.fr.
181 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX354166 958 bp mRNA linear EST 08-APR-2004 BX354166 Homo sapiens NEUROBLASTOWA COT 25-NORWALIZED Homo sapiens CDNA clone CS0DC015YH04 5-PRIME, mRNA sequence.
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/db xref="taxon:9606"
/clone="CSODCOISATOMA COT 25-NORMALIZED"
/tissue type="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                             GGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTG
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GGGTGCCGAGGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCA
                               GGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 958)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Contact: Genoscope
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Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1094)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Lupublished (2001)

On May 8, 2003 this sequence version replaced gi:30452476..

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX376199 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC024YAl0 5-PRIME, mRNA sequence.
                                                GGTGCCGAGGCCCGATGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAG
                                                                                                                                                                                  GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC
                                                                                                                                                                                                                                                                                                                                      GAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCAACCTGGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAG
                                                                                                                                                                                                         CGGGGGAATATCCTGATTCCGGGTCTCCCCAGAAGCCCATCAGTAGCTTTGGTTTTT
                                                                                                                                                                                                                                                                                                    641 CGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT
                                                                                                                                                                                                                                                                                                                                                                               701 GAGCGCCACTICCTGCCAACCAATCGAAATCGGAMTGTAGGAGCCAMCCGGCTCAAMCAR
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DC024YA10"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Br 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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ALS59769 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CSODG005YF11 5-PRIME, mRNA sequence.
                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 999)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                division of Invitrogen.

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODGOO5CCO6QPl&c=7766.r.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Homo sapiens"
                                                          AL559769.3 GI:46185141
                                                                                             Homo sapiens (human)
Homo sapiens
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Matches 913; Conserv
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/organism="Homo sapiens"
/mol type="mRNA"
/db_tref="taxon:9606"
/db_tref="taxon:9606"
/clone="INAGE:544101"
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/clone_lib="NIH MGC:98"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dr priming. Directionally cloned into BcoR1/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                     BM910587 12-MAR-2002
AGENCOURT 6702754 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5454101
5', mENA Sequence.
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1031)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conteact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1948 row: I column: 06
High quality sequence stop: 679.
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Pred. No. 1e-241;
0; Mismatches 7; Indels 1
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Matches 931; Conservative
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    /tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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      at:
    I.M.A.G.E. Consortium/LLNL
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L Similarity 97.5%; Pred. No. 1.7e-239;
965; Conservative 0; Mismatches 21;
found through the I.M.A.G.E. Conson
http://image.llnl.gov
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
E. (Dases i to 1019)
S. NIH-MGC http://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT 6491037 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723623 5', mRNA sequence.
BMS46877 GI:18780186 EST.
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            GGCAGCCCAGAGCAACCTGGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACA
                                   GCCAGCCCAGAGCAACCTGGGCTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACA
                                                                                                                               ATCTACCAGGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTATCCGA
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AL518361 ALO SADIENS 1016 bp MRNA linear EST 23-MAR-2004 AL518361 Homo Sapiens NEUROBLASTOMA Homo Sapiens cDNA clone CSODA009YD01 5-PRIME, mRNA Sequence.
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                                                       CAGGAGCTGGTCGTCTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCGACCTCCACCTC
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                   CAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCTCCTGTTTGTCCTGGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.gemoscope.cns.fr/cdna?s=CSODK002CA10QP1&c=7766.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gi:30614376.
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COT 25-NORMALIZED Homo
mRNA sequence.
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|cell_line="HELA"
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Pred. No. 3.5e-239;
3; Mismatches 0;
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Genoscope - Centre National de Sequencage
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978 bp
BX400806 Homo sapiens HELA CELLS of the cond clone CSODK002XB19 5-PRIME, BX400806
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'db_xref="taxon:9606"
'clone="CS0DK002YB19"
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larity 99.2%;
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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RESULT 14 BX400806

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1016)

1. (bases 1 to 1016)

1. Wh. B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

1. Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:30536600.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EWRY cedex - France

BP 191 91006 EWRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see thttp://www.genoscope.cns.fr/cdna?s=CSODA009CB01QP1&c=7766.r.
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="texon:9606"
/clone="CSODAQOSYDO1"
/rissue type="NEUROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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Search completed: November 10, 2004, 18:18:00 Job time : 3883.13 secs

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ADC23337 standard; DNA; 1115
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Adc60227 Human mic
Adc60229 Human mic
Adc60229 Human KNS
Adk40995 Novel hum
Adc2334 Human ENS
Adc2334 Human ENS
Adc2334 Human Encod
Adc2334 DNA encod
Adc60231 Human mic
Adc60231 Human mic
Adc44493 Human Gen
Ach77408 Human Gen
Ach71108 Human Gen
Ach71108 Human Gen
Ach61108 Human Gen
Adc1108  DNA encod
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Aba94616 Nucleotid
Abs57216 DNA encod
Aba94614 Human kin
                                                             November 9, 2004, 09:45:10; Search time 576.523 Seconds (without alignments) 10152.424 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   4134886 seqs, 2624710521 residues
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Maximum Match 100%
Listing first 45 summaries
                                         - nucleic search, using sw model
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## ALIGNMENTS

BP

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/*tag= a
/product= "KID protein"
/product= except= (pos: 1..5; aa: Met)
/note= "This codon has an apparent 2 nucleotide insertion
that alters the reading frame"
                                                                                                                          DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 1).
                                                                                                                                                                                       human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodilator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
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20-JUN-2000; 2000US-00597292.
                                                         18-DEC-2003 (first entry)
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                                             This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length
                                                                                                                                                                                                                                                                                                                                                                  CGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC 120
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directly/indirectly produces ADP or phosphate.
                        Disclosure; SEQ ID NO 1; 26pp; English
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activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, and act as a modulator of the binding characteristics or biological activity of a tracting receiv, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and inflammation, for treating cellular proliferation disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders and inflammatory bowel disease and angioplasty. This sequence respectable in coding a human microtubule motor protein of the invention. Note: The specification states that this armaar received the protein featured as SEQ ID NO:2, but this does not
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/note= "This codon has an apparent 1 nucleotide deletion
that alters the reading frame"
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                                                                                                                         TGGCCCCATTTGCCCAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG
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ACCAGCGCTCCTCCCCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTT
                                                                                       TGGCCCCATTTCGCCAGCGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGG
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28-NOV-2000; 2000US-00724224.
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                                 This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular conformation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor composed in modulating the activity of target proteins having motor or phosphate. Purthermore, this activity can be determined using cor phosphate. Purthermore readouts. The present invention describes a method that identifies modulators of the target protein, which is a ckinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene content treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 3) encoding a full length con a composition.
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Pred. No. 1.1e-310;
0; Mismatches 1; Indels
    or phosphate
                       Disclosure; SEQ ID NO 3; 26pp; English
    produces ADP
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Matches 1113; Conservative
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cc proteins, method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target corporation or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular complexation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune chiesas, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and candioplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention. Note: The specification states that this sequence encodes the protein featured as SEQ ID NO:4, but this does not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for modulating the expression of
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                                                                            ACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGGGGGAGCCATCAACACCT
                 721 ACCAGCGCTCCCCCCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAAAGTT
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comprising anothering the interaction of THAP, responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragament with a muchaic acid, and so enhancing or repressing comprises modulating the expression of a gene rapsonsive to a THAP/chemokine of modulating the expression of a gene responsive to a THAP/chemokine complex; (1) a pharmaceutical comprision comprising a THAP-family of a THAP responsive element; (4) a cell comprision of complex; (5) a transcription factor decoy consisting the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or its biological fragment or a nucleic acid and a THAP-family polypeptide or a proposition associated with a condition mediated by a THAP-family polypeptide in an individual; (1) methods of identifying a test compound that modulates transcription changing associated with transcription associated with a condition mediated by a THAP-family polypeptide in an individual; (1) a vector or insufficient appropriate associated with transcription mediated by a THAP-family polypeptide in an individual; (1) a comprising a detectable product; (12) a genetically engineered cell comprising a man and an RHAP family polypeptide in an individual; (1) a modulation mediated by a THAP-family polypeptide in an individual; (1) a man individual or a polypeptide that does not be product; (12) a genetically appropriated that a polypeptide in an ind
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GACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCC 365 207 245 CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAG 305 66 ATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCA 125 GATCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAAC 267 CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAG 327 GCCGCGGCGCCTCCACCACCACAGGCGACGCGAGATGGCGGCAGCTTCAGCGGCGCG 65 28 eccecedecrecarcecadas de casa de constante de constant GATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAAC Gaps 99.3%; Score 1107.4; DB 12; Length 2097; 99.9%; Pred. No. 3.4e-309; ive 0; Mismatches 1; Indels 0; C Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other; Conservative Query Match Best Local Similarity Matches 1108; Conserva φ 148 186 208 246 268 306 126

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269 CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAG 328
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                                                                                                                                                          389 AGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACAATGCTGGGCAGCACA
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                                              GACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and encodes a naturally occurring kinase polypeptide; (d) encodes the conjugation of an id), except that it lacks one or more, but not all, of an complement of complement of an actalytic domain, a catalytic domain, a catalytic domain, a cuterminal domain, a coiled-coil structure region, a spacer region and a C-complement of a catalytic domain, a C-complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or cutronal-associated diseases, and metabolic disorders. The disorders are controlar or peripheral nervous system, Alzheimer's disease, brain, controlar or peripheral nervous system, Alzheimer's disease, corrections, infections caused by tions, infections caused by fungi, ocular diseases, migraines, pain, conteria, infections caused by fungi, ocular diseases, migraines, pain, conteria, infections, hypertension, psychotic disorders, contition disorders, dyskinesias, metabolic disorders and organ transplant controlation. This sequence corresponds to the DNA encoding one of the
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metabolic disorder; organ transplant rejection; enzyme; gene;
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99.3%; Score 1107.4; DB 10
Best Local Similarity 99.9%; Pred. No. 3.4e-309;
Matches 1108; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 33; SEQ ID NO 102; 491pp; English.
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     gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
wound; infectious disease; ss.
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cellular proliferation disorder; cancer; hyperplasia; restenosis;
cardiac hypertrophy; immune disorder; inflammation.
Kinesin-like DNA binding protein; KID; autoimmune disease; arthritis;
graft rejection; inflammatory bowel disease; angioplasty.
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 1038; Conservative 0; Mismatches
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                                           20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
         28-NOV-2000; 2000US-00724224
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                                                                                               (CYTO-) CYTOKINETICS INC
                                                                                                                                                                       WPI; 2003-706919/67
                                                                                                                                                                                        P-PSDB; ADC23342.
                                         20-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as and inflammation, for treating disorders associated with kinesin-like DNA condining protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular condining protein disorders and inflammation, for treating disorders concer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune consisted with KID and for inhibiting KID and for thibiting KID and for thibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted with KID and for inhibiting KID and for treating autoimmune consisted angioplasty. This sequence represents DNA encoding a human microtubule angioplasty. This sequence represents DNA encoding a human microtubule
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100.0%; Pred. No. 2.9e-289;
ive 0; Mismatches 0;
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Matches 1038; Conservative
                                            CYTOKINETICS INC
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P-PSDB; ADQ60232.
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                                                                                                664 AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human microtubule motor protein #4"
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                               This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity of an bedtermined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunoancodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynuclecide sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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                                                                                      Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1035.4; DB 10; Length 1464;
Pred. No. 1.9e-288;
0; Mismatches 1; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                              Disclosure; SEQ ID NO 7; 26pp; English.
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Best Local Similarity 99.9
Matches 1036; Conservative
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening corrections of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor corrections, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or correction or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or correction, and methods of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders second inflammation, for treating disorders associated with kinesin-like DNA correcting for modulators of motor proteins useful for treating callular correcting for modulators of motor proteins useful for treating callular correcting for modulators of motor inflating KID. The sequences are used for screening for modulators of motor proteins useful for treating autoimmune disorders and inflammation, for treating autoimmune confiscated with KID and for inhibiting KID and for treating autoimmune confiscated with KID and for inhibiting KID and for treating autoimmune confiscated with KID and for inhibiting KID and for treating autoimmune confiscated with KID and for inhibiting KID and for treating autoimmune confiscated with KID and for inhibiting KID and for treating autoimmune confiscated with KID and for inhibiting KID and for treating and indicated after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule contor protein of the invention.
New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                                                      Disclosure; SEQ ID NO 7; 26pp; English
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Gaps 92.9%; Score 1035.4; DB 12; Length 1464; 99.9%; Pred. No. 1.9e-288; ive 0; Mismatches 1; Indels 0; ( Best Local Similarity 99.9 Matches 1036, Conservative Query Match

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                                     GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGGGAGCAAGTGATCCCCCCTGT 197
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                                                                                                                                                              GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC
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           GTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT
                                                                                           CTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGAGTACTCAGCAGGACATCTATGCA
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Claim 1; SEQ ID NO 31705; 44pp; English.

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The invention relates to an isolated polynuclectide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (EST) for information, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 464 BP; 96 A; 136 C; 131 G; 96 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/sequence.html?DocID=20030073623
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

03-APR-2002; 2002US-00029386 03-APR-2002; 2002US-00029386

US2003194704-A1 16-OCT-2003. Claim 15; SEQ ID NO 10603; 80pp; English

surveying tissues.

Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration. derived single exon probe #10603. ACH77408 standard; DNA; 531 BP. (first entry) Human genome 29-JUL-2004 ACH77408; RESULT 13 

Homo sapiens

817 818 GATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAA 877 758 CAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGGAAAACTCTACCT 34 CCAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGGAAAACTCTACCT Gaps ; 0 Matches 235; Conservative Local Similarity 94 셤 ð 셤 ò

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and equences in the specification. The probe is a single axon probe that the relationship of the specification. The probe is a single axon probe that the relationship of single daressed in human cells or tissues. Also included are a spatially. A spressed in human cells or tissues. Also included are a spatially of expressed in human cells or tissues. Also included are a spatially of addressable set of single exon nucleic acid probes for measuring human gene expression, a method of and addressably isolatable or amplifiable from the plurality, a single contiguous amino acids of any of the above- mentioned amino acid subscription, and configuous amino acids of any of the above- mentioned amino acid solutions and/or licensing single exon probes or microarray to record sequences (optionally with conservative amino acid substitutions), an extend of sealing and/or licensing single exon probes or microarrays to a customer destring to measure gene expression, a method of providing methods of sealing and/or licensing single exon probes or microarrays to a customer destring to measure gene expression of a single exon probe of the probe, methods and datables that purelity of records to record including data on the expression of a single exon probe of the probes may be used as tools for surveying trisques to detect the presence of expressed measages that contain their caperonic the probes may be used as tools for surveying trisques to detect the presence of expressed measages that contain their capecting and characterising grows a literative splicing events, in detecting and characterising of a human gene expressing the Order prope are used in identifying and characterising and characterising and expressing the genomic locus that includes their expressing Score 233.2; DB 12; Length 531; Pred. No. 8e-57; 0; Mismatches 3; Indels 0; Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other; 20.9%; Query Match 

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences this defined in the specification. The probe is a single exon probe that this defined in the specification. The probe is a single exon probe that the expression (comprising a plurality of probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wettor comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe contiguous amino acids of any of the above—mentioned amino acid of solated on the specifically to a peptide cited above, and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing contrage medium which contains a database having a plurality of records cited above. The probe, methods and apparatum are useful in gene expression analysis. The probes may be used as tools for surveying cited above. The probe, methods and apparatum are useful in gene expression analysis. The probes may be used as tools for surveying cited exon, or in constructing genome-derived single exon microarrays.
AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 937
                    New human genome-derived single exon nucleic acid probes useful for hume gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                      reagggcrecercergracerrareggacacacaacacacercecerarecaggae 995
                                                                                            Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                          Human genome derived single exon probe #24303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 24303; 80pp; English
                                                                                                                                                                                                              ACH91108 standard; DNA; 232 BP.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                          942 GGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
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                                                                                                                                                                                           DB 12; Length-232;
                                                                                                                                                                                                                         1; Indels
                                                                                                                                                           Sequence 232 BP; 55 A; 64 C; 68 G; 45 T; 0 U; 0 Other;
                                                                                                                             segdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                          Score 230.4; DB 1;
Pred. No. 3.6e-56;
0; Mismatches 1;
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Seki N, Yoshikawa T,
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P-PSDB; ADM04007.
                                                                                                                                                                                                          Similarity
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as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM03154 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
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                                        Score 184.6; DB 11; Length 2095;
Pred. No. 1.6e-42;
0; Mismatches 379; Indels 21;
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Sequence 2095 BP; 489 A; 603 C; 658 G; 345 T; 0 U; 0 Other;
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Search completed: November 10, 2004, 06:57:50 Job time : 582.523 secs

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Cloned into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
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Full-length cDNA libraries and normalization
Unpublished
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/tjone="CSODIO40Y106"
/tissue type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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AUTHORS
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Oy 4 GGTCGCTGTCGCCTAACAAATTGAACTAA 	1084 GTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGCCGAGGCCCT 1143 	& 8
Query Match Best Local S Matches 1456	1024 AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGACCT 1083 1029 AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGACCT 1088	à à
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/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:966" /clone="CSOD1009YJ01"	904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963	oy Db
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- Web : WWW.genoScope.cus.ll)  COMMENT 1st strand cDNA was primed with a end enriched, double-strand cDNA w into the Not I and EcoR V sites of	784 AACAAGGGCCTTCGGCTAAAAGAGGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGC 843 	A G
AUTHORS Genoscope.  IITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope BP 191 91006 EVRY cedex - FRANCE (	724 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACCGGCGCACAGGC 783 	VO QQ
REMARK Contact: Feng Liang Email: illan http://fulllength.invitrogen.com/ Faraday Avenue Faraday Avenue 2 (bases 1 to 2025)	664 AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGGGGAACGTTTGGCCCCATTTCGCCAG 723 	상 유
REFERENCE 1 (bases 1 to 2025) AUTHORS Li,W.B., Gruber,C., Jessee,J. and TITLE Full-length cDNA libraries and nor JOURNAL Unpublished	604 CTGCCAGCCAGTCGAATCGCACTGTAGGAGCCACCCGGCTCAACCAGGGCTCTCCGGC 663	λδ Dp
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of Homo Bapiens (human) CR590974. CR590974.1 GI:50471781 HTC: CNSLT GDNA.	484 GACCTCCTGGACCCTGCTTCGGGGGACCTGGTAATCCGAGAAGACTGCCGGGGGGAATATC 543 	ଧ ଶ
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	RESULT 4 AK084310 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	AUTHORS AUTHORS . TITLE JOURNAL	MEDLINE PUBMED REPERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
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AL Nature 420, 563-573 (2002)

State (bases 1 to 2055)

Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, C., Mateuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, A., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sapazume, N., Sogabe, Y., Tanaka, T., Tomaru, K., Shinagawa, A., Shiraki, T., Takaku, Muramatau, M., and Hayashizaki, Y., Yasunishi, A., Toya, T., Yasunishi, A., Direct Submission Hayashizaki, T., Yasunishi, A., Direct Submission Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@ggc.riken.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Pred. No. 1.2e-273;
0; Mismatches 227; I
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/db_xref="taxon:10090"
/clone="D230020105"
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8. .1991
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/strain="C57BL/6J"
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/cell type="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
1.2056
/note="kinesin superfamily protein KIF22"
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                         prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. .2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 1063.6; DB 3;
83.9%; Pred. No. 1.5e-272;
iive 0; Mismatches 230;
                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/64"
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/db_xref="taxon:10090"
/clone="2400004116"
                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.9
Matches 1201; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujiwake, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Miramatsu, M., Inoue, K., Tanaka, T., Matsuura, S., Kawai, J., Riken integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (202)
6 (bases 1 to 2056)
                                                                            AK075922 2056 bp mRNA linear HTC 03-APR-2004 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2400004116 product:kinesin superfamily protein KIF22, full
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                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhe RIKEN Genome Exploration Research Group Phase II Team and
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-560 (2001)
                                                                                                                                                                                                                                                                                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                       AK075922.1 GI:26096579
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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pCMVSPORT 6 vector. Library
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                 was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7766.r
                                                                                                                                                                                                                          /tissue type="Piacenth COT 25-NORMALIZED"
/clone lib="Homo sapiens Placenth COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI009CE01QP1&c=7766. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  68.8%; Score 1007; DB 1; Length 1124; 96.9%; Pred. No. 1.7e-257; ive 25; Mismatches 5; Indels 2.
and EcoR V sites of the p
Library was constructed
                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1009YJ01"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Peb 15, 2001 this sequence version replaced gi:31267547.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVNY cedex - France
BP 191 91006 EVNY cedex - France
Bmail: seqref@genoscope.cns.fr, Neb: www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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AL545712.3 GI:45746191
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
           AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGGGCGCACAGGAAACTCTACATTGATTTGGCTGGTTCAGAGGACAACCGTCGCACGGAAACTCTACATTTGGCTGGTTCAGAGGACAACCGTCGCACGGCAA
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BX337353 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI040XI06 5-PRIME, mRNA sequence.

BX337353
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVNY codex - France
BP 191 91006 EVNY codex - France
BP 191 squeef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Enail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
end enriched, double-srrand cDNA was digested with Not I and cloned
into the Not I and Ecoa V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                              BX337406
BX337406 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COTOR CSODIO41XII3 5-PRIME, MRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (1001)
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        AACAAGGGCCTTCGGCT-AAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGG
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODIO41AE07QP1&c=7766.r.
hctp://www.genoscope.cns.fr/cdna?s=CSODIO41AE07QP1&c=7766.r.
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3; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1031)

S NIH-MCC http://mgc.ndi.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1948 row: 1 column: 06

High quality sequence stop: 679.
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_6702754 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5454101
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          GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
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/tissue_type="Astrocytoma grade IV, cell line"
/lab host="DH10B (phage_resistant)"
/clone_lib="NIH_MGC_98"
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/db_xref="taxon:9606"
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                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1032)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

1 Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30337600.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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  GI:46272059
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                                                                                                                                                                                                                                                                     CAGAATGCCAGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTG
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                                                                                                                                                                                                   GGAGCAAGTGATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAAC
                                                                                                                            Gaps
                                                                                                                         1;
                                                                                                      Length 1031;
                                                                                                                          Indels
                                                                                                      63.0%; Score 922.4; DB 4;
larity 99.0%; Pred. No. 6.7e-235;
Conservative 0; Mismatches 8;
                                                                                                                   Best Local Similarity
Matches 937; Conserv
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into /organism="Homo sapiens"
/mol\_type="mRNA"
/db xref="taxon:960s"
/db xref="taxon:960s"
/clone="cSonGoSYLI1"
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/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 123 188 183 248 243 303 128 02-APR-2004 63 AL559772 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG005YL11 5-PRIME, mRNA sequence.
AL559772 GI:46185144 CTCAAATACCAGTTTGATGCCTTCTATGGGGAGGAGTACTCAGCAGACATCTATGCA GGTCGCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGAAGG GTGGCTGTGCGCACTGCGGCCATTTGTGGAAGGAACAGCGGGAGCAACTGATCCCCCCTGT GTGCGGGGCATGGACAGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGAATGCCAGTGTGCTTGCC GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG Gaps 4 Length 1083; 1047 946 Indels 62.3%; Score 912.8; DB 1; larity 96.1%; Pred. No. 2.5e-232; Conservative 13; Mismatches 21; Homo sapiens (human) Homo sapiens Similarity Query Match Best Local Simil Matches 942; ( EST. 249 69 64 129 124 189 184 244 901 1003 source

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Library was not normalized."
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end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoRV sites of the pCNVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, division of Invitrogen.

This sequence belongs to sequence cluster 7766.r

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODA009CBOIQPI&c=7766.r.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                    Length 1016
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                                                                                                                                                                                                                                                                                                                                                 61.3%; Score 897; DB 1; I. larity 98.5%; Pred. No. 4.1e-228; Conservative 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 923; Conserv
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Genoscope - Centre National de Sequencage
BPP 191 91006 EVNY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL518361 Homo sapiens NEUROBLASTOWA Homo sapiens CDNA clone CSDA009YD01 5-PRIME, mRNA sequence.
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GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC 368
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unil-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:30536600.
                                                                                         GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
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                              TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG
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BX363358 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CSODK012YE23 5-PRIME, mRNA sequence.
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                                             GAGGAGGTGCCGAGGCCCGGCCATTGTGTCACCACCATGTCTTACCTAGAGATC
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into EccRI; cDNA made by oligo-dT priming. Directionally cloned
into EccRI; cDNA made by oligo-dT priming 5, adaptor:
GGCAGGAG(G): Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT_7026550 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5932716
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LLCM2116 row: b column: 13
High quality sequence stop: 690.
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Pred. No. 2.5e-224;
0; Mismatches 23; Indels 13;
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999; Conservative (
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into EccRI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
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AGENCOURT 7025845 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935518
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NH-WGC http://mgc.nni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
          CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAGGTATTA
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Plate: LLCM2123 row: g column: 07
High quality sequence stop: 660.
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I (bases 1 to 959)

I (bases 1 to 959)

Ei, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30368690.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NoI-oligo(dT) primer

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .959
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BP 191 91006 EVRY cedax - France
Email: sequencacope.cns.fr, Web : www.genoscope.cns.fr
Ist strand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized: Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                      958 bp mRNA linear EST 08-APR-2004
BX354166 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC015YH04 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 958)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015YH04"
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                                                                                                                                                                                               Homo sapiens (human)
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BC073177 Xenopus I
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Db 241 GGAACCACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTC 300  Qy 301 AGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGA 360  Db 301 AGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGA 360	Qy 361 ATGCCAGTGTGCCTATGGACCCACAGAGGGGCTGGGAAGACGCACACAATGCTGGGCA 420	OY 421 GCCCAGAGCAACCTGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGG 480	Oy 481 AGGAGGTGCCGACGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCT 540	OY 541 ACCAGGAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAAG 600	OY 601 ACTGCCGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTG 660	OY 661 ATTITGAGCGGCACTTCCTGCCAGCCGAAATCGGACTGTAGGAGCCACCGGGTCA 720	OY 721 ACCAGGGTCCTCCCGCAGTCATGCTGTCCTGGTCAAGGTGGACCAGCGGGAACGTT 780	QY 781 TGGCCCCATTTCGCCAGCGAGAGGGAAAACTCTACCTGATTGACTTGGGTCAGGGG 840	OY 841 ACAACCGGGGCACAGAGGACCTTGGGCTAAAAGAGAGTGGAGCCATCAAAACT 900	OY 901 CCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGCCTCCCTC	QY 961 ATCGGGACAGCTCACTCGCCTATTGCAGACTCTCTGGGTGGCTCACCCACAGTA 1020	OY 1021 TCCTTATTGCCAACATTGCCCCTGAGAGGCTTCTACCTAGACACAGTCTCGGCACTCA 1080	QY         1081 ACTTIGCTGCCAGGTCCAAGGAGGTGATCAATTGA         1115           Db         1081 ACTTIGCTGCCAAGGAGGTGATCAATTGA         1115		LOCUS AR210053 1538 bp DNA linear PAT 20-JUN-2002 DEFINITION Sequence 3 from patent US 6387644. ACCESSION AR210053.1 GI:21512183		REFERENCE 1 (bases 1 to 1538) AUTHORS Beraud. 7. TITLE Motor proteins and methods for their use JOURNAL Patent: US 6387644-A 3 14-MAY-2002;	

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                                                                                                                                                                                                                        GCCGCGGCGCTCGACGCAGCAGCGGACGCGAGATGGCGGCAGCTTCAGCGGCGCG
                                                                                                                                                                                                                                                                               66 ATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCA
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Pred. No. 2.6e-276;
0; Mismatches 1; 1
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Best Local Similarity 99.9%;
Matches 1108; Conservative
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Kalnine, N., Chen X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Koundinya, M. and Farmer, A.

Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Ling Tay, M. and Farmer, A.

Ling Submitteed (13-MAY-2020) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TW) cloning system between the Sall and HindlII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindlII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                       1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,W., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Chelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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GSEDDRRTGBKGLRLKESGAINTSLEVLGKVVDALNOSLPRVPYBDSKUTRLLQDSLG
GSABILIIANIAPERRFYLDVVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKE
LLGPPEAKRARGPEEEEIGSPEPMAAPASASOKLSPLOKLSSMDPANLERLLSLDRIL
ASQGSQGAPILSTPKRERMVLMKTVEEKDLEIERLKYKQKELEAKMLAQKAEEKENHC
                                                                                                                                  1021 TCCTIATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA 1080
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WAVRLRPPYDGTAGASDPCYRGMDSCSLEIANWRHNGTLEXYQFDAFYGERGTQQD
IYAGSVQPILRHLLESQNASVLAYGFTGAGKTHTMLGSPEQPGVIPRALMDLLOLTRE
EGAEGRPWALSVTMRYLEIYQEKVLDILDPASGDLVIREDCRGNILIPGLSQRFSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9506"
/db_xref="Hou245X1.0"
/clone="GH00245X1.0"
/clone=lib="BD Creator(TM) CDS Library derived from MGC
                                                  TCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA
                                                                                                                                                                                                                                                                                                                                    BT007259 1998 bp mRNA linear
Homo sapiens kinesin-like 4 mRNA, complete cds.
BT007259
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/note="Vector: pDNR-Dual"
                                                                                                                                                                                       ACTITIGCTGCCAGGTCCAAGGAGGTGATCAATTG 1114
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/protein id="AAP35923.1"
/db xref="GI:30583357"
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FLI_CDNA.
Homo sapiens (human)
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AUTHORS
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JOURNAL
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PTWLRPLSHRTVTGAKPLKKAVVMPLQLIQEQAASPNAEIHILKNKGRKRKLESLDAL
EPBEKAEDCWELQISPELLAHGRQKILDLINEGSARDLRSLQRIGPKKAQLIVGWREL
HGPPSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGASL"
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                                                                                                     Length
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                                                                                                 12;
                                                                                               Score 1107.4; DB 12
Pred. No. 2.6e-276;
0; Mismatches 1;
                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 1108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATC' to provide Kozak consensus sequence, 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
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RVAVRIRPFVOGTAGASDPPCVRGMDSCSLEIAWRNHGETLKYQFDAFYGERSTQO
TYGSVOPILRHLIAGQNASVILAYGPTGAGKTHTWILGSPEQPCVIPRALMDLIQLTRE
EGAEGRPWALSVYWYYLEIYOBKYLDILDPAGGDLVIREDCKGNILIPGLSQKPISSF
ADFERHPLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLA
GSEDNRRTGNKGLRIKESGAINTSLFVLGKVVDALNQSLPRYPRDSKLTRLDQSLG
GSEDNRRTGNKGLRIKESGAINTSLFVLGKVVDALNQSLPRYPRDSKLTRLLDGSLG
GSAHSILIANIAPERRFYLDTVGALHVARARGPEEBIGSVGKLSQKE
ILGPPEAKRARGPEEBIGSPERMAAPASAGQKLSPLCKLSGKLSGKLSGKLSCHC
ASQGSQGAPLLSTPKRERMVLMKTVEEKDLEITRLKTKQKELEAKMLAQKAEBKENHC
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 1998)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                     BT007888 13-MAY-2003
Synthetic construct Homo sapiens kinesin-like 4 mRNA, partial cds.
BT007888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 1998)
2 (bases 1 to 1998)
3 (kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinyar, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
                                                                                       ATTGCCAACATTGCCCCTGAGAGGCCTTCTACCTAGACACAGTCTCCGCACTCAACTTT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived from MGC
                            GACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTT
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|transl_table=11
|product="Homo aspiens kinesin-like
|protein id="AAP36560.1"
|db_xref="GI:30584615"
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note="Mutations: 1997:Stop->Leu"
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/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
                                                                                                                                                                                          GCTGCCAGGTCCAAGGAGGTGATCAATCG 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="GH00245L1.0"
/clone_lib="BD Creator(TM)
collection"
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Homo sapiens mRNA for kinesin-like DNA binding protein, complete
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Direct Submission

Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Tokyo, The Institute of Medical Science, Department of Oncology, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan (E-mail:tokai@hqc:ims.u-tokyo.ac.jp, Tel:03-5449-5302, Pax:03-5449-5413)

D38751:Submitted (02-Nov-1994)
Sequence updated (25-Peb-1999).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         GAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGGTCAACAG
                                 568 GAGAAGTATTAGACCTCCTGGACCCTCGGAGGAGACCTGGTAATCCGAGAAGACTGC
                                                                                                                                       688 GAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCACCGGCTCAACCAG
                                                                                                                                                                            CGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCC
                                                                                                                                                                                           GACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGGTGGCTCAGCCCACAGTATCCTT
                                                                                    CCATTTCGCCAGCGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1048 ATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACACGTCTCCGCACTCAACTTT
                   GAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC
                                                                    CGGGGGAATATCCTGATTCCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT
                                                                                                                                                                                                                                                                                  GACAGCAAGCTCACTCGCCTATTGCAGGACTCTGGGTGGCTCAGCCCACAGTATCCTT
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AB017430.2 GI:4519442
Kid; kinesin-like DNA binding protein; kinesin family.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                       SM Unknown.

Unclassified.

Unclassified.

I (bases 1 to 2097)

S Beraud, C., Ohashi, C., Sakowicz, R., Vaisberg, E., Wood, K. and Yu, M. Human kinesins and methods of producing and purifying human kinesins

Rinesins

RL Patent: US 654466-A 34 08-APR-2003;

Location/Qualifiers

1. 2097

/organism="unknown"
/mol_type="genomic DNA"
                                                   GATCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAG
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                                                                                                                                                                                                     linear
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                                                                                                                                                                                               AR304057 2097 bp
Sequence 34 from patent US 6544766.
AR304057 GI:31692955
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Best Local Similarity 99.9
Matches 1108; Conservative
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Strausberg, R.L., Feingold, E.A., Grouse, D.H., Derge, J.G., Klausner, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Morley, K.C., Hale, S.J., Mosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Butterfield, Y.S., Krzywinski, M.I., Skalakka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Onose, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC028155
Homo sapiens kinesin family member 22, mRNA (cDNA clone MGC:40049
IMAGE:5241557), complete cds.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2117)
                                                                                               688 GAGCGCCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCCCCCGGCTCAACCAG
                                                                                                                                                                        748 CGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCC
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Best Local Similarity 99.9
Matches 1108; Conservative
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                                                                                                                    USA

WIN-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapGs-romail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Contact: MGC help desk
Email: cgapGs-romail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Gaithersburg, Maryland;
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haqhighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,B.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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                            Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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6. .2003
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Pred. No. 2.6e-276;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pooled"
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Best Local Similarity 99.9%;
Matches 1108; Conservative 0
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AUTHORS
TITLE
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 8 BC004352

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ACCESSION

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Matches 1108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L. UGBERG 1. L. Felingold, E. A., Grouse, L. H., Derge, J. G., Strauberg, R. L., Felingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Colling, F. S., Wagner, L., Schemen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Morce, T., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Staplecon, M., Soares, W. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J. Uddin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Morenan, R. J., Mallahy, S. J., Boasak, S. A., McDwan, P. J., McKernan, K. J., Mallek, J. A., Garkis, P. H., Richards, S. W., Vilalon, D. K., Malek, J. A., Sodergren, E. J., Lu, K. Gibbs, R. A., Vilalon, D. K., Marny, D. M., Sodergren, E. J., Lu, X. Gibbs, R. A., Fahey, J., Halton, E., Ketteman, M., Madan, A., Young, A. C., Shevchenko, Y. Boutfard, G. G., Blakesley, R. W., Trouchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov series: 18ALD Flate: 8 Row: £ Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Feathbristone, Maleni Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, MS Santos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                   2134 bp mRNA linear PRI 29-JUN-2004
nily member 22, mRNA (cDNA clone MGC:1573
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
   Homo sapiens kinesin family m
IMAGE:3535435), complete cds.
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REFERENCE AUTHORS TITLE JOURNAL PUBMED

REMARK COMMENT

JOURNAL

TITLE

/organism="Homo sapiens" /mol\_type="mRNA"

1. .2134

source

FEATURES

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                                                                                        OBP-1, OBP-2, KNSL4"
/clone="MGC:1573 IMAGE:3535435"
ftissue type="Lung, small cell carcinoma"
/clone_lib="NIH MGC_7"
/lab_host="DHJOB-R"
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99.9%; Pred. No. 2.6e-276;
iive 0; Mismatches 1;
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Qy         198         GTGCGGGGATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGAT         257           Db         124         GTGCGGGGATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAAACCACGAGGAACATTGTTAACTGCAACAGCAACAGGAAGACT         183	w 0	GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC	Qy         378 TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG         437	Qy         438         Grantcccccccccccccccccccccccccccccccccccc	Qy         498 CGGCCATGGGCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 557           Db         424 CGGCCATGGCCTTTCTGTCACCATGTCTTACCTAGAGATATTA 483	QY         558 GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC 617           DD         484 GACCTCCTGGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC 543	0y         618         CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTTGAGCGGCACTTC         677           Db         544         CTGATTCCGGGTCTCTCCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC         603	Qy         678         CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCCCGC         737           Db         604         CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCCCGC         663	QY         738 AGTCATGCTGCTCCTGGTCAAGGTGGACGGGAACGTTTGGCCCCATTTCGCCAG         797           Db         664 AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCAGGAACGTTTGGCCCCATTTCGCCAG         723	0y 798 CGAGGGAAAACTCTACCTGATTGACTTGGGTCAGGGGACAACGGGGGCACAGGC 857	Oy 858 AACAAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGC 917	QY         918 AAAGTGGTAGATGGGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCTC 977           DD         844 AAAGTGGTAGATGCGCTGAATCAGGCCTCCCTCGTGTACCTTATCGGGACAGCTC 903	Oy   978 ACTICGCCTATTGCAGGACTCTCTGGGGTGGCTCAGCCACAGTATCCTTATTGCCAACATT 1037	Qy   1038 GCCCCTGAGAGGCTTCTACCTAGACAGGTCTCCGGACTCAACTTTGCTGCCGGGGTCC 1097	Qy         1098 AAGGAGGTGATCAATTGA 1115           Db         1024 AAGGAGGTGATCAATTGA 1041	AR210055 1464 bp	DEFINITION Sequence 7 from patent US 6387644. ACCESSION AR210055. GI:21512186 KEYWORDS . SOURCE Unknown.
Qy         546 GAGAAGGTATTAGACCTCCTGGACCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC         605           Db         563 GAGAAGGTATTAGACCTCCTGGACCTGGTCGGGAGAACCTGGTAATCCGAGAAGACTGC         622	Qy 606 CGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT 665	QY       666 GAGCGGCACTTCCTGCCAGCCAGCCAGCGGGCCACCGGGTCAACCAG       725         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 726 CGCTCCTCCCGCAGTCATGCTGCTCCTGGTCAAGGTGGACCAGCGGAACGTTTGGCC 785	Oy 786. CCATTICGCCAGCGAGAAAACICTACCTGATIGACTIGGCTGGGTCAGAGGACAAC 845	OY 846 CGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTG 905	Oy 906 ITTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTC	Qy     966     GACAGCAAGACACACCTCTATTGCAGGACTCTCTGGGTGGCTCACCCACAGTATCCTT     1025       Db     983     GACAGCAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTT     1042	QY 1026 AITGCCAACATTGCCCCTGACAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTT 1085	Qy         1086 GCTGCCAGGTCCAAGGAGTGATCAATTG         1114           Db         1103 GCTGCCAGGTCCAAGGAGTGATCAATCG         1131	טר חאת יירוביו מאת מל 2011	NN Sequence 5 from patent US 6387644.  1 AR210054.1 GI:21512185	SOURCE Unknown. ORGANISM Unknown. Unclassified.	AUTHORS Beraud, C.  IIILE Motor proteins and methods for their use JOURNAL Patent: US 638764-A 5 14-MAY-2002; FRATHRES	Й	Query Match 93.1%; Score 1038; DB 6; Length 1041; Best Local Similarity 100.0%; Pred. No. 2.6e-258; Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 78 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCCACCTCCAGGTCGCGTAAGG 137	Oy 138 GTGGCTGTGCGACTGCGGCCATTTGTGGATGGGAGGGAGG

Db 844 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCT Qy 978 ACTCGCCTATTGCAGACTCTCTGGGTGGCTCA Db 904 ACTCGCCTATTGCAGACTCTCTGGGTGGCTCA Qy 1038 GCCCCTGAGAGACGCTTCTACCTAGACACACTC Db 964 GCCCCTGAGAGACGCTTCTACCTAGACACACTC OV 1098 AAGGAGGTGATCTACTACCTAGACACACTC OV 1098 AAGGAGGTGATCTATCTACCTAGACACACTC		RESULT 11           BC003427 BC003427 BC003427 C086 bp   DCUS BCO03427 PAGE BD BCO03427 PAGE BD BCO03427 PAGE BD BCO03427 PAGE BD BCO03403 P	197 ACCESSION VERSION	257 ALTIMOKUS SOURCE ORGANISM	317 REFERENCE 243 AUTHORS	377	437	497	TATTA 557 BOUNDARY S.Y.W., JOHN BOUNDARY S.Y. Grim Butterfield, Y.S., Krzywinski, M.I., Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schein, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schoin, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schoin, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schoin, J.B., Jones, S.J. TATTA 483 Schnerch, A., Schoin, J. Tatta 483 Schnerch, A., Schoin, J. Schoin, J. Tatta 483 Schnerch, A., Schoin, J. Schoi	617 JOURNAL 543 PUBMED	677 REFERENCE TITLE TITLE TOURNAL	737 . REMARK 663 . REMARK	GCCAG 797 COMMENT Contact: MGC help desk GCCAG 797 Tassue Procurement: Jeffrey Green M GCCAG 723 COMMENT Library Preparation: Life Tech	857		843	977
ORGANISM Unknown. Unclassified.  Unclassified.  Discrepance 1 (bases 1 to 1464)  AUTHORS Beraud.C.  TITLE Motor proteins and methods for their use JOURNAL Patent: US 6387644-A 7 14-MAY-2002; FEATURES  Location/Qualifiers  source /organism="unknown" /mol_type="unassigned DNA"	Ouery Match 92.9%; Score 1035.4; DB 6; Length 1464; Best Local Similarity 99.9%; Pred. No. 1.2e-257; Matches 1036; Conservative 0; Mismatches 1; Indels 0; C	Oy 78 GGTGGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCTCCAGCTCGCGTAAGG 	OY 138 GIGGCICIGCCACTGCCGCCATTGTCCATGCAACACGGGAACAAGTGATCCCCCCTGT	Oy 198 GTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACGGGAGACT	Oy 258 CTCAAATACCAGTTTGAIGCCTTCTATGGGGAGAGAGTACTCAGGAGGACATCTATGCA	OY 318 GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGAATGCCAGTGTGCTTGCC	OY 378 TATGGACCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG	Oy 438 GTGATCCCGCGGCCTCTCATGGACCTCCTGCAGCTACAAGGGAGGG	Qy 498 CGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA	Qy 558 GACCTCCTGGACCCTGCTTCGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC	Qy 618 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGGGGACTTC	OY 678 CTGCCAGCCAGTCGAATCGGACTGTAGGAGCCACCCGGCTCAACCAGGGGTCCTCCCGGC	Qy 738 AGTCATGCTGCTCCTGGTCAAGGTGGACCAGGGGAACGTTTGGCCCCATTTCGCCAG 	Oy 798 CGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAGG	858	784	Qy 918 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTC

Grouse, L.H., Derge, J.G.,
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ow, K.H., Schaefer, C.F., Bhat, N.K.,
T., Max, S.I., Wang, J., Hateh, F.,
mer, A.A., Rubin, G.M., Hong, L.,
I.do, M.F., Casavant, T.L.,
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I.do, M.F., Toshiyuki, S.,
S., Loquellano, N.A., Peters, G.J.,
Sak, S.A., McEwan, P.J.,
Sak, S.A., McEwan, P.J.,
M., Gay, L.J., Hulyk, S.W.,
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M., Gay, L.J., Hulyk, S.W.,
M., Gay, L.J., Rodrigues, S.,
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Touchman, J.W., Green, E.D.,
Touchman, J.W., Green, E.D.,
Trimwood, J., Schmutz, J., Myers, R.M.,
T., Stalska, U., Smailus, D.E.,
S.J. and Marra, M.A. rerecgeacreaacritigergecaggrec 1097 CAGCCCACAGTATCCTTATTGCCAACATT 1037 mRNA linear ROD 29-JUN-2004 r 22, mRNA (cDNA clone MGC:6456 , X., Hulyk, S.W., Loulseged, H., R.G., Muzny, D.M., Nanavati, CTCGTGTACCTTATCGGGACAGCAGCTC 903 niata; Vertebrata; Euteleostomi; urognathi; Muridae; Murinae; Mus. Institutes of Health, Mammalian omics Office, National Cancer 11A03, Bethesda, MD 20892-2590, chnologies, Inc. A.G.E. Consortium (LLNL) of Medicine Human Genome (26), 16899-16903 (2002) ci.nih.gov .edu/cdna/

600 658 99 718 780 838 840 898 900 958 960

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Buxaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151041)
1 (bases 1 to 151041)
2 (bases 1 to 151041)
3 Eirran, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Andern, B., Linton, L., Nusbaun, C., Lander, E., Ali, A., Allen, N., Bairran, B., Linton, L., Nusbaun, C., Changuiavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Calima, S., Collymore, A., Cook, A., Cook, P., Dewar, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferraira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Gord, S., Gord, S., Gord, S., Gord, S., Hulme, W., Illev, I., Johnson, R.,
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Mus musculus clone RP24-158A6, WORKING DRAFT SEQUENCE, 4 unordered
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AC101919.4 GT:28951338
HTG; HTGS_PHASR1; HTGS_DRAFT.
MNB musculus (house mouse)
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TITLE
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181.
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Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C.,
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 150741; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 150558 bases at least Q30 Consensus quality: 150654 bases at least Q30 Consensus quality: 150654 bases at least Q20
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Web site: http://www-seq.wi.mit.edu
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JOURNAL
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AUTHORS
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COMMENT

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55488 ACTCAGTGGGACATCTATGTAGGTTTAGTACAGCCCATACTAAGGAACTTGCTGGAAGGG 65429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCAGCCCAGAGCAACCTGGGGTGATCCCGGGGGCTCTCCATGGACCTCCTGCAGCTCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 ACTCAGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGG
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    contig of 33517 bp in length 100 bp 100 bp in length 100 bp in length 100 pp in contig of 41558 bp in length 100 to 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in length 100 bp in
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of 33517 bp in length
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Pred. No. 9e-166;
0; Mismatches 206;
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Best Local Similarity 79.7
Matches 844; Conservative
                                             33518
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Sirren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J.,

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Contact: sequence submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-24 Male Mouse BAC" 1. .1655

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Center clone name: 344_C_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             64891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953 TGTACCTTATCGGGACAGCAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCACC 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1013 CCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGGCGCTTCTACCTAGACACAGTCTC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC101752 164759 bp DNA linear ROD 23-APR-2004
Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
AC101752
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                                                                                                                                                                                                                                                     836
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 16475)
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                                                                                                                                                                                                                                                                                      CAACACCTCCTGTTTGTCCTGGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64710 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAA 64672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAA 1111
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Mus musculus chromosome 1, clone RP24-344C18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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AC101752/c
LOCUS
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VERSION
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AUTHORS
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19260. .19949
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20118. .20297
/rpt_family="MLT1D"
complement(20386. .20639)
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20634. .20839
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/rpt family="Li MM"
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2115. .2157

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'xpt_family="(TTC)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 AGGGAGGAGGGTGCCGAGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAG 536
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1748 63847; gap of 100 bp

1848 73892; contig of 10045 bp in length

173922; gap of 100 bp

1851 154560; contig of 80458 bp in length

1851 157808; contig of 1358 bp in length

1851 167808; contig of 1358 bp in length

1809 167908; gap of 100 bp

17611; contig of 8803 bp in length

17611; gap of 100 bp

17611; gap of 100 bp

1812 233800; contig of 56689 bp in length

1801 233800; gap of 100 bp

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78.1%; Pred. No. 1e-158;
...rive 0; Mismatches 223; Indels
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------ Project Information
Center project name: L17732
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/clone_lib="RPCI-24 Male Mouse BAC"
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Web site: http://www-seq.wi.mit.edu
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/organism="Mus musculus'
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/db_xref="taxon:10090"
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953 TGTACCTTATCGGGACAGCAGGAGGTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGC 1012
                                                                                                                                                                                                                                                                                                                                                                                                       1013 CCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC101908
297639 bp DNA linear HTG 18-JUN-2004
Mus musculus chromosome 1 clone RP24-275J1 map 1, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 297639)
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                                                                                                                  145122 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAA 145084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACI01908.4 GI:44199137
HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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Mus musculus chromosome 1, clone RP24-275J1
Unpublished
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KEYWORDS
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M Mus Euk Mam	A Bir Mus Unp	REFERENCE 2 (bases 1 to 196674)   GGAAGGG 356	416	476 791	536 731	596 671	656 611 TITLE	716 JOURNAL REFERENCE 551 AUTHORS	GGGAA 776 Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,  Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J.,  Choepel, Y., Collymore, Cook, A., Cooke, P., Corum, B.,  ATGAA 491 BeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,	836 · ·	GAGCCAT 892  GAGCCAT 892  MacLean,C., Macdonald,P., Major,J., Manning,J., Mathews,C., McCarthy,M., Maldrim,J., Meneus,L., Mihowa,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,	952 311	Stojanovic, N., Stubbs, M., Talamas, J., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., TCAGC 251  Zimmer. A. and Zody, M.	1072 TITLE JOURNAL	CAATCTC 191 REFERENCE 4 (bases 1 to 196674) AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boustayki, V., Boukhqalter, B., Camarata, J., Chang, J.,
177 GGAGCAAGTGATCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCT	237 TGGAGGAACCACCAGGACACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGG 	297 ACTCAGCAGACATCTATGCAGGTTCAGTGCCAGCCCATCCTAAGGCACTTGCTGGAA 	AGAATGCCAGTGTGCCTATGGACCCACAGAGGAGTGGAAGACGCACACACA	417 GGCAGCCCAGAGCAACCTGGGGTGATCCCGGCGCTCTCATGGACCTCCTGCAGCTCACA	477 AGGAGGAGGGCCCAGCCATGGCCCTTTCTGTCACCATGTTTACTAGAG	537 ATCTACCAGGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGA 	597 GAAGACTGCCGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTT	657 GCTGATTTTGAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGG	717 CTCAACCAGCGCTCCTCCGGAGTCATGCTGTGCTCCTGGTCAAGGTGGACAGCGGGAA 	777 CGTTTGGCCCATTTCGCCAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCA 	837 GAGGACAACCGGGGCACAGGGCCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGC 	893 CAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGGGGTGAATCAGGGCCTCCCTC	953 IGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGC	1013 CCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACAGAGT	250 TCAIAGCAICCTCAITGTCAGCAITGCTCCTGAAAGATGTTTTTACCTGGAIACAAT 1073 CGCACTCAACTTTGCTGCCAGGTCCAAGAGGTGATCAA 1111

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chasco, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Conder, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gordes, P., PitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Garden, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landerst, T., Lehoczky, J., Levine, K., Liu, G., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Mathova, T., Munga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., Pollara, V., Norwan, C.H., O'Connor, T., O'Donnell, P., Pollara, V., Sawert, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seerery, P., Spencer, B., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, 
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Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Bloom, T., Bogulalavkiy, L., Boukhgalter, B., Canarata, J., Chang, J.,

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Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,

Erickson, J., Rato, S., Rerreira, P., FitzGerald, M., Gage, D.,

Radagan, J., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,

MacLean, C., Macdonald, P., Manjor, J., Matthews, C.,

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Romann, J., Schauer, S., Schupback, R.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Zimmer, A. and Zody, M.

Direct Submission

Submitted (10-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

H. (Dases I to 19667)
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Biren, B., Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barra, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barra, N., Bastien, V., Bloomel, Y., Collymore, A., Cooke, P., Conum, B., Choepel, Y., Collymore, A., Cooke, P., Conum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faros, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnes, C., Kamat, A., Karatas, A., Kals, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Mucphy, T., Naylor, J., Nguyen, C., Nguyen, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Neil, D., Oliver, J., Peterson, K.,
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AC102127 19674 bp DNA linear ROD 01-MAY-2004 Mus musculus chromosome 1, clone RP23-202A19, complete sequence.

Mus musculus (house mouse)

GI:46931440

AC102127 AC102127.11 HTG.

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 15 AC102127 LOCUS

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repeat_region
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         Retta. R., Rise, C., Royov. P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasaliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission

L. Submitted (101-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 1, 2004 this sequence version replaced gi:46358225.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                       Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
Center project Information
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
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101632 TTTATGACTATGCCCATTTATGGATGAAGAAAAAAAAGGAAAGGGATGCCCTTGTGTAAG 101691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
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Pred: No. 1.3e-124;
0; Mismatches 242;
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complement(13221..13381)
/rpt_family="B3A"
13437..13578
15222..15254
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complement(16922..17052)
/rpt_family="B4"
17101..17490
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complement (9243. .9815)
/rpt family="L1"
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complement(15315..15605)
/rpt_family="RMER20"
complement(16008..16517)
/rpt family="RMER15"
complement (6185, .627)
/rpt famil
                                /rpt_family="RSINE1"
6516. .657^
                                                                                  /rpt_family="(T)n"
complement(6571..6823)
/rpt_family="L1_MM"
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17725. .17762
'rpt_family="(GGAA)n"
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/rpt_family="(TG)n"
16809. .16866
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007. ,7285
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292. .7848
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Best Local Similarity 74.4%;
Matches 726; Conservative
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102408 AAGTGGAGGTTGCATCATATTAGGGCTCCCTCCTATATTATACTGGGACAGAAAATCA 102467
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                  101992 GGCCATGGGACATTTCTGTCAGGATGTCCTATTTAGAGGTCTACCAGGAAAAGGTATTAG 102051
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                                                                                                                                                                                                                                                                                                                                                                                                                              799 GAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859 ACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCA 918
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                                                                    GGCCATGGGCCCTTTCTGTCACCATGTCTACCTAGAGATCTACCAGGAGAAGGTATTAG 558
439 TGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGCC 498
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                                                                                                                                                                                                                                                                                   679 TGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCCGCA
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Search completed: November 10, 2004, 13:17:54 Job time: 4934.36 secs

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November 10, 2004, 13:18:18; Search time 781.387 Seconds (without alignments) 10087.639 Million cell updates/sec
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| Cgn2 6/ptodata/1/pubpna/US06 MmP DuB.seq:*
| Cgn2 6/ptodata/1/pubpna/US06 MmP DuB.seq:*
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| Cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
| Cgn2 6/ptodata/1/pubpna/US0 O_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de					
Result No.	Score	Query	Query Match Length DB ID	DB	QI .	Description	
-	1464	100.0	1464	17	17 US-10-797-893-7		
71	1461	99.8	1538	17	US-10-797-893-3	Sequence 3, Appli	
m	1447	98.8	2099	16	US-10-334-143-102		
4	1443.2		2104	σ	US-09-925-300-288		
S	1038.4		1041	17	US-10-797-893-5		
9	1035.4		1115	17	US-10-797-893-1		
7	480		491	σ	US-09-960-253-131		
80	376.4	25.7	386	10	US-09-803-719-1937	Sequence 1937, Ap	
6	365		24525	13.	US-10-087-192-1180		
10	265		464	10	US-09-918-995-31705		
11	262.4		24291	13	US-10-087-192-1177		
12			531	'n	115-10-029-386-10603		

	Sequence 201, App Sequence 22135, A Sequence 2359, Ap Sequence 46568, A Sequence 34, Appl Sequence 34, Appl Sequence 27001, Appl Sequence 762, Appl Sequence 762, Appl
US-10-029-386-24303 US-10-108-260A-249 US-10-28-226-301 US-09-883-096-1 US-09-883-096-6 US-10-437-963-1460 US-10-437-963-1460 US-10-425-139A-498 US-10-425-139A-498 US-10-425-139A-498 US-10-425-139A-498 US-10-425-135-48 US-10-425-135-48 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-313-642-3 US-10-316-472-23 US-10-316-472-23	US-10-104-047-201 US-10-425-114-2135 US-10-739-930-2359 US-10-425-115-46568 US-10-133-937-34 US-10-159-563-34 US-10-169-493-27001 US-10-104-047-762 US-10-172-118-1053
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1464;
             Sequence 7, Application US/10797893
Publication No. US20040142397A1
GENERAL INPORMATION:
APPLICANT: Beraud. Christophe
TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 1464; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1464
US-10-797-893-7
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Sequence 102, Application US/10334143

Sequence 102, Application US/10334143

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: MINASES IDENTIFIED WITH THE METHOD

FILE REFERENCE: 038602/1543

CURRENT FILING DATE: 2002-12-31

PRIOR PELLING DATE: 2001-12-31

SROCHWARE: PARENTIN NUMBER: 60/343,169

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PARENTIN Ver. 2.1

SEQ ID NO 102
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98.6%; Score 1443.2;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1450; Conservative 7; Mismatches
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                                                                             ) NAME/KEX: misc feature
) COCATION: (44)
) OTHER INFORMATION: n equals a,t,g, or
) LOCATION: (497)
) OTHER INFORMATION: n equals a,t,g, or
) LOCATION: (1323)
) OTHER INFORMATION: n equals a,t,g, or
US-09-925-300-288
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                                   TYPE: DNA
ORGANISM: Homo B
FEATURE:
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US-09-925-300-288

; Sequence 288 Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REPERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR PLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIN Ver. 2.0
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TITLE OF INVENTION: Novel motor proteins and met
TITLE OF INVENTION: their use
FILE REPERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASLEEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10797893
Publication No. US20040142397A1
GENERAL INFORMATION:
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Best Local Similarity
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TYPE: DNA
ORGANISM: Human
S-10-797-893-5
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CICCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGA 1055
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                                                                       CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGGGACAACCGGCGCACAGGC
                                                                                                         798 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC
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; Patent No. US20020123619A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Dodes, Michael J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.556
; CURRENT APPLICATION NUMBER: US/09/960,253
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.8%; Pred. No. 2.3e-138;
Matches 491; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
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                                                            Sequence 1, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
   APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICANION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/9/724,224
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR APPLICATION NUMBER: 09/597,292
; RILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; TANGTH. 11-16
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larity 99.9%; Pred. No. 8e-311;
Conservative 0; Mismatches 1; In
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US-10-797-893-1
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Best Local Simi
Matches 1036;
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                                                                                                                                                 241 GTACCCCAAAGCGAGAGGGGATGGTGCTAATGAAGACAGTAGAAGAAGGACCTAGAGA 300
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                                                                                                                                                                                                                                      301 TTGAGAGGCTTAAGACGAAGCAAAAAAAAACGAACCTGGAGGCCAAGATGTTGGCCCAGAAGGCTG 360
121 CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGC 180
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                                                                                  181 GCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGGCCCCTCTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 AGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGGAGAGACTGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 24525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.29452001122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377
FRICH APPLICATION NUMBER: US 09/747,377
FRICH APPLICATION NUMBER: US 09/798,586
FRICH FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 2059
SEQ ID NOS: 2059
SEQ ID NO 1180
LENGTH: 24525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%; Score 365; DB 13; 73.8%; Pred. No. 5.1e-102; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   1433 AGGAAAAGGAGAACCATTGTCCCACA 1458
                                                                                                                                                                                                                                                                                                                            361 AGGAAAAGGAGAACCATTGTCCCACA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 1180, Application US/10087192; Publication No. US20020182586A1
GENERAL INFORMATION: APPLICANT: MORTIS, David W.
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Matches 597, Conservative
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; ORGANISM: Homo sapiens
US-10-087-192-1180
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                                                                                                                                               419
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APPLICANT: Labat, Ivan
APPLICANT: Kita, David
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1644.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT APPLICATION NUMBER: 00/188,609
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.4%; Pred. No. 3.3e-106;
Matches 380; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1937, Application US/09803719
Publication No. US20030044783A1
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominiquez
APPLICANT: Sudduth-Kiinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Rendazzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Lamson, Ceorge
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
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                                                                                                                     GCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGTCTACCAGGAGAAGGTATTAGA 485
                                                                                                                                                                                      CCTCCTGGACCCTGCTTCGGGAGACTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT 545
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                                                                      2999 GGAACATCCTGATCCCAGGCCTCACAGAAGCCCATCACCAGCTTCTCTGACTTCGAGC
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217 CGGTGCCTGAGGAGCTGCATTAC-ATCTCGATGCTTGGCAGCCCAGAGCAACCTGGGGT
                                                      rgcagctcacaagggaggagggggggggggggg
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                                                                                                                                                                                                                                                                                                                                                        Sequence 1177, Application US/10087192
; Sequence 1177, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INPORMATION:
    APPLICANT: Bengelhard, Eric K.
    TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
    FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF ERQ ID NOS: 2059
; SOFTWARE: FastesQ for Windows Version 4.0
; SEQ ID NO 1177
; LENGTH: 24291
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Best Local Similarity 73.8%; Pred. No. 3.9e-70;
Matches 385; Conservative 0; Mismatches 61;
                                                         GAICCCGCGGGCTCTCAIGGACCICCI
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Mus musculus
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US-10-087-192-1177
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                                                                         ATCAACACCTCCCTGTTTGTCCTGGCCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCT 2792
                                                                                                                                CCTAGACACACTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCC 1043
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            GGGTCAGAGGACAACCGGCGCACAGGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCC 2732
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                CGTGTACCTTATCGGGACAGCACAGCTCACTCGCCTATTG-----
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18.1%; Score 265; DB 10;
Best Local Similarity 77.6%; Pred. No. 1.5e-71;
Matches 333; Conservative 0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTACCAATGAGAGCCTGCAGCCTCATG 1072
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; CTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705
                                                                                                                                                                                      ORGANISM: Homo sapiens
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LENGTH: 464
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APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION: EXPRESSION ANALYSIS TWO CURRENT APPLICATION NUMBER: US/10/029,386; CURRENT FILING DATE: 2001-12-20; NUMBER OF SEQ ID NOS: 34286; SOUTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 24303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO CHRI6.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIT: 014807, EVALUE 5.00e-37
OTHER INFORMATION: BST HUMAN HIT: BE382882.1, EVALUE 1.00e-125
US-10-029-386-24303
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Pred. No. 1.2e-46;
0; Mismatches 379; Indels
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 99.6
Matches 231; Conservative
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Matches 464; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Pean, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Pance, David R.
APPLICANT: Pance, David R.
APPLICANT: Savid R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERBYNCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                            3359 AACACCICCITITGIACIGGCAAAGIGGGGGATGCATIAAACCAGGGCCTCCCICGC 3418
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                                                                                                                                                                                                                                                                                                                                         TCAGAGGACAACCGGCGCACAAGAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATC
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: WISSPROT HIT: Q14807, EVALUE 2.00e+30
OTHER INFORMATION: EST_HUMAN HIT: BF975048.1, EVALUE 1.00e-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3419 ATACCATACCGGGACAGCAAGCTCACTCGTCTGCTGCAGGTC 3460
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Publication No. US20030194704A1
GENERAL INFORMATION:
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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Best Local Similarity 98.7°
Matches 235; Conservative
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LENGTH: 531
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APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zhong, Mei
TITLE OF INVERTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT PILING DATE: 2002-11-04
FRIOR FILING DATE: 2002-11-30
FRIOR PILING DATE: 2002-03-04
FRIOR PILING DATE: 2002-03-04
FRIOR PILING DATE: 2002-02-04
FRIOR APPLICATION NUMBER: 60/346,000
FRIOR APPLICATION NUMBER: 60/346,000
FRIOR APPLICATION NUMBER: 60/344,000
FRIOR PILING DATE: 2002-03-03
FRIOR PILING DATE: 2002-03-03
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Spytek, Kimberley A.,
Taupier, Jr., Raymond J.
Vernet, Corine A.M.,
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                                                                                                                                                  Macbougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Millet, Isabelle,
Ooi, Chean Eng,
Ort, Tatiana,
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Malyankar, Uriel M.,
MacDouqall, John R.,
Kekuda, Ramesh,
Khramtsov, Nikolai,
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Rastelli, Luca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rieger, Daniel K.,
Rothenberg, Mark E
Shenoy, Suresh G.,
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ORGANISM: Homo sapiens
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    CCCACAGAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATC 369
                                                                             406 cccacadecreredegaaaaccracarecraecraedecacaccadeaecredecarcrar 465
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CAACGACCTCTTCCGTGCCATCGAGGACCAGCAATGA-----CATGGAGTATGA 722
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                                                                                                                                                                   321 TGGGAAGACGCACACAATGCTGGGCAGCCAGAGCAACCTGGGGGTGATCCCGGGGGCTCT
                                                                                                     Gaps
                                                                   Query Match
Best Local Similarity 54.1%; Pred. No. 1.3e-37;
Matches 395; Conservative 0; Mismatches 317; Indels 18;
; NAME/KEY: CDS
; LOCATION: (7)..(3351)
US-10-287-226-301
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Sequence 301, Application US/10287226 Publication No. US20040086875A1

RESULT 15 US-10-287-226-301

GENERAL INFORMATION:

APPLICANT: Ages, Michele L.,
APPLICANT: Ages, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Edinger, Andrew,
APPLICANT: Blerman, Karen,
APPLICANT: Gangolli, Esha A.,
APPLICANT: Gangolli, Esha A.,
APPLICANT: Garlach, Valerie,
APPLICANT: Garlach, Valerie,
APPLICANT: Garlach, Valerie,
APPLICANT: Garlach, Valerie,

See File Wrapper or PALM

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972 GAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGT 1031
                                                                                                                                     1263 dagcagrecerregagagerecegaaeaeeeergaeeraeeeegeeeggeeaagaar 1322
681 GGTCAAGGIGGACCAGCGGAACGTTT---GGCCCCATTTCGCCAGGGGAAAACT 737
                                                                                                                         738 CTACCTGATTGACTTGGCTGAGGACAACCGGCGCACAGGCAACAAGAGGCCTTCG 797
                                                                                                                                                                                       858 GCTGAATCAGG-----GCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCT 911
                             843 CGAAGTCTCCACCATCAATGCCAAGGATCATGCAGCTGCTGATGAAGGGGAACCGGCA 902
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ORGANISM: Human
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Best Local Simi:
Matches 1464;
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US-09-724-224-7
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US-09-724-224-7
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(cgn2_6/ptodata/1/ina/RECTUS_COMB.seq:*

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Sequence 7, Application US/09724224;
Patent No. 6387644;
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6387644el motor prot
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT APPLICATION NUMBER: 09/597,292
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR APPLICATION NUMBER: 09/597,292
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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                                                                  ; Sequence 7, Application US/10093317; Patent No. 6762043; GENERAL INFORMATION: Batent No. 6762043; GENERAL INFORMATION: APPLICANT: Beraud, Christophe; TITLE OF INVENTION: No. 6762043el motor proteins and methods for; TITLE OF INVENTION: their use; FILE REFERENCE: 1044; CURRENT APPLICATION NUMBER: US/10/093,317; CURRENT FILING DATE: 2002-03-06; PRIOR PILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 8; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 7.
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Best Local Similarity 100.
Matches 1464; Conservative
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                                            Score 1461; DB
Pred. No. 0;
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Best Local Similarity 100.
Matches 1461; Conservative
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     ; TYPE: UNA
; ORGANISM: Ht
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GGCAAAGTGGTAGTGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAAG
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; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: 09/597,292
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR PLING DATE: 2000-11-28
; SOFTHARE: FastSEQ for Windows Version 4.0
; SGO ID NO 3
; LENGTH: 1538
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	APPLICANT: Beraud, Christophe APPLICANT: Beraud, Christophe APPLICANT: Bakewicz, Roman APPLICANT: Sakewicz, Roman APPLICANT: Waisberg, Eugeni APPLICANT: Wood, Kenneth APPLICANT: Wood, Kenneth APPLICANT: Wing TITLE OF INVENTION: Human kinesins and methods of producing TITLE OF INVENTION: and purifying human kinesins TITLE OF INVENTION: and purifying human kinesins TITLE OF INVENTION ON HORER: US/09/595,684B CURRENT FILING DATE: 2002-06-24 PRIOR APPLICATION NUMBER: 09/295,612 PRIOR APPLICATION NUMBER: 09/295,612 PRIOR APPLICATION NUMBER: 09/295,612 PRIOR APPLICATION ON HORER: 2000-04-20 SEQ ID NOS: 105 SEQ ID NOS: 105 SEQ ID NO 34 LENGTH: 2097 TYPE: DNA TYPE: DNA CORGANISM: Human US-09-595-684B-34	Ouery Match         99.6%; Score 1458; DB 4; Length 2097;           Best Local Similarity         100.0%; Pred. No. 0;         0; Indels         0; Gaps         0;           Matches 1458; Conservative         0; Mismatches         0; Indels         0; Gaps         0;           Op         4 GGTCGCTGCTCGCCTCCACCTCCACCTCCACCTCGCGTAAGG         63         100 GGTCGCTGTCGGCTAAGTAGGAAGTTCGTCACCTCCACCTCCACCTCGGTAAGG         159           Op         64 GGTGGCTGTGCGCCTATTGTGGAACTACTCGTCGCCCCTCCACCTCGGTAAGG         159           Op         140 GTGGCTGTGCGACTGCGCCCATTGTGGAACAGCGGGAACACTCCCCCCTGTT         219           Op         124 GTGGCTGTGCGACTGGGCCCATTGTGGAACAGCGGGAACCACCCCGGGAACT         279           Op         124 GGTGGGGCTTGGAACAGTGCTCTCTAAGGGGGAACACTCAGGAACACCCAGGAACT         279           Op         124 GGTGCGGGCATTGAAGCCTCTCTAAGGGGAACACTCAAGGAACACTCAAGGAACACTCAAGAACACCAGGAACACTTATGCA         239           Op         220 GTGCGGGGATTGATGATGCTTCTATGGGGAACACTCAAGAGAACACCAAGAACTCAAGAACACTCAAGAACACTCAAGAACACTCAAGAACACTCAAGAACACTCAAGAACACTCAAGAACACAATGCAAGAACACTCAAGAACACAAATACAAGAAATACAAGAAATACAAATACAAGAAATACAAATAACAAATACAAATAACAAATACAAATAACAAATACAAATAACAAATAACAAATAACAAAATAACAAATAACAAATAACAAATAACAAAATAACAAAATAACAAAAAA

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US-10-093-317-5
US-10-093-317-5
; Sequence 5, Application US/10093317
; Sequence 5, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; TITLE OF INVENTION: No. 6762043el
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT PILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 5
; SEQ ID NO 5
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70.9%; Score 1038.4; DB 4; Length 1041;
Best Local Similarity 99.9%; Pred. No. 8.8e-293;
Matches 1039; Conservative 0; Mismatches 1; Indels 0;
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; ORGANISM: Human
US-10-093-317-5
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y Sequence 5. Application US/09724224
y Patent No. 6387644
y General INFORMATION:
y TITLE OF INVENTION:
y FILE REFERENCE: 1044
y CURRENT APPLICATION NUMBER: US/09/724,224
y CURRENT FILING DATE: 2000-11-28
y PRIOR PAPLICATION NUMBER: 09/597,292
y PRIOR PLING DATE: 2000-06-20
y NUMBER OF SEQ ID NOS: 8
y SOFTWARE: FeatSEQ for Windows Version 4.0
y SEQ ID NO 5
y LENGTH: 1041
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Pred. No. 8.8e-293;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1039; Conservative
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ORGANISM: Human
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; Batent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT PILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-6-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENTH: 1115
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; Sequence 1, Application US/09883096
; Batent No. 6680369
; GENERAL INFORMATION:
; APPLICANT: Baraud, Christophe
; APPLICANT: Sakowicz, Roman
; APPLICANT: Sakowicz, Roman
; APPLICANT: Partel, Umesh A.
; APPLICANT: Davies, Katherine A.
; APPLICANT: Davies, Katherine A.
; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
; TITLE OF INVENTION: UNVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
; CURRENT APPLICATION NUMBER: US/09/883,096
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 6
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PATENTIN VET. 2.1
                                                                                                                              784 AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGC
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9.5%; Score 138.6; DB 4; Length
Best Local Similarity 51.0%; Pred. No. 4.8e-30;
Matches 448; Conservative 0; Mismatches 404; Indels
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                                                                                                ; Sequence 1, Application US/10093317; Patent No. 6762043; Patent No. 6762043; GENERAL INFORMATION: F. TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use; FILE REFERENCE: 1040.

CURRENT APPLICATION NUMBER: US/10/093,317; CURRENT PILING DATE: 2002-03-06; PRIOR APPLICATION NUMBER: 09/724,224; PRIOR APPLICATION NUMBER: 09/724,224; PRIOR PILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 8; NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1035.4; DB.4; Length 1115;
Pred. No. 6.9e-292;
0; Mismatches 1; Indels 0;
                 1098 AAGGAGGTGATCAATTG 1114
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Best Local Similarity 99.9%;
Matches 1036; Conservative
                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-093-317-1
                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 1115
                                                                                          US-10-093-317-1
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                                                                                                                                                                                                                                                                                      27;
   OTHER INFORMATION: Description of Artificial Sequence: HsKip3a OTHER INFORMATION: fragment OTHER INFORMATION: Nucleotide sequence of HsKip3a fragment used OTHER INFORMATION: ATPASE assay (Figure 5).
                                                                                                                                                                                                                          Length 1152
                                                                                                                                                                                                                   Score 136.6; DB 4; Length
Pred. No. 9.5e-30;
0; Mismatches 389; Indels
                                                                                                                                                                                                               Query Match
Best Local Similarity 51.2%;
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APPLICANT: Yu, Ming
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APPLICANT: Parel, Umesh A.
APPLICANT: Davies, Katherine A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REPERENCE: 020552-00.1400S
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIN Ver. 2.1
LENGTH: 1152
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Patent No. 6680369
GENERAL INFORMATION:
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ORGANISM: Human
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sequence 1, Application US/09621233
patent No. 6294371
general information:
APPLICANT: Beraud. Christophe
APPLICANT: Beraud. Christophe
TITLE OF INVENTION: No. 6294371e1 motor proteins and metl;
TITLE OF INVENTION: their use
FILE REFERENCE: 1080;
CURRENT APPLICATION NUMBER: US/09/621,233
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 897
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; Patent No. 636841
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6368841el motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: USO90724,508
; CURRENT APPLICATION NUMBER: 108/09/724,508
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/621,233
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NOS: 2
; SEQ ID NOS: 2
; SEQ ID NOS: 2
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Pred. No. 1.6e-27;
0; Mismatches 356;
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964 GCCCCTGAGAGACGCTTCTACCTAGACAGTCTCCGCCACTCAACTTTGCTGCCAGGTCC 1023
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                                                      Query Match

8.8%; Score 128.8; DB 4; Length 897;
Best Local Similarity 50.1%; Pred. No. 1.6e-27;
Matches 430; Conservative 0; Mismatches 356; Indels 72
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; OTHER INFORMATION: n = a, c, t, or US-10-090-695-1
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AC092562 Papio ham
AB017335 Homo sapi
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Patent: US 6387644-A 7 14-MAY-2002;
Location/Qualifiers
1. .1464
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                              DNA
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Sequence 7 from patent US 6387644.
AR210055
AR210055.1 GI:21512186
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                                                                     AB017333S2
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AC122863
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AX833125
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AL929469
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1 (bases 1 to 1464)
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Beraud, C.
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Best Local Simi
Matches 1464;
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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FEATURES
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BT007808 Synthetic
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BC004352 Homo sapi
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AC101908 Mus muscu
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1 atgggtcgctgtcggctaag......accattgtcccacaatgtga 1464
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       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Salaine, N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalaine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Woreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteonics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion TW)
cloning system between the Sall and Hindill sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'Hiddill site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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HGPFSQVEDLERVEGITGKQMESFLKANILGLANGCAS"
1 (bases 1 to 1998)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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116 GOTTOMOGRACIO CONTROLINA CONT		A NOI S	_	JOURNAL Unpublished  REFERENCE 2 (bases 1 to 1998) AUTHORS Kalnine, M., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Roundinya, M., and Farmer, A.  TITLE Direct Submission JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow	CITCLE, FAIO ALCO, CA 79309, 036  This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the expression clones generated by BD Biosciences Clontech and the farvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'Acc' after Sall site	last codon and before HindIII site to maintain reading frame.  Clone distribution: http://bioinfo.clontech.com/orfclones. Location/Qualifiers Source /organism="synthetic construct" /mol_type="mRNA" /db_xref="textoness" /location-mcMn024510"	/clone_libe=BD Creator(TM) CDS Library derived from MGC collection" /lab host="DHSalpha T1 resistant" /note="Vector: pDNR-Dual" 1>1998 /note="Mutations: 1997:Stop->Leu" /codon start=1	/trails_Lant-lano sapiens kinesin-like 4" /product="Homo sapiens kinesin-like 4" /protein_id="AAP186560.1" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /db_cref="G1:30584615" /rdccref="G1:30584615" /rdccre
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Tokai-Nishizumi,N. and Edamasu,M.

Direct Submission

Bubmitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Tokyo, The Institute of Medical Science, Department of Oncology;

4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan (B-mail:tokai/appc.ims.u-tokyo.ac.jp, Tel:03-5449-5302,

Bar:03-5449-5413)

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10.60   GCCCCTGAGAGACGCTTCTACCTAGACACTCCGCACTCCAACTTTGCTGCCCCGGGTCC   1119   111	BC028155  BC028155  Homo sapiens kinesin family member 22, mRNA (cDNA clone MGC:40049)  IMAGE:5241557), complete cds.  BC028155  BC028155  GC028155  GG1:20380446  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  SS Straubberg, Metzeora, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.  1 (bases 1 to 2117)  S Straubberg, L., Schebrg, B. Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. P., Collins, F. S., Wagner, L., Schaefer, C. F., Bhat, N. K., Hopkins, R. P., Jordan, H., Moore, T., Was, S. I., Wagner, T. L., Schaefer, C. F., Bhat, N. K., Hopkins, R. P., Jordan, H., Moore, T., Was, S. I., Wagner, T. L., Scheets, T. E., Brownstein, M. J., Uddin, F. B., Toshiyuki, S. Scheetz, T. E., Brownstein, M. J., Uddin, F. L., Toshiyuki, S. K., Marano, K. J., Malek, J., Garcia, A. M., Gay, L., J., Hulyk, S. W., Wallalon, D. K., Wallah, S., Garcia, A. M., Gay, L., J., Hulyk, S. W., Willalon, D. K., Wallah, Madan, A., Young, A.C., Shewchenko, Y., Bouffert, J. Hulyk, S. W., Willalon, D. K., Wallah, Madan, A., Young, A.C., Shewchenko, Y., Boufferd, G. G., Blakesley, R. W., Touchman, J. W., Geen, E. D. Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myes, R. M., Butterfield, Y. S., Kzzywinski, M., Salsky, U., Samilus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Garcia, A. A. Boufferd, S. Garcia, M. A. Gay, L., Salsky, M. Schein, J. E., Jones, S. J. and Marra, M. A. Garcia, J. Hulyks, S. W. Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Garcia, J. M. A. Gay, L., Schnerch, J. Walland, S. J. Garcia, J. Salsky, M. S
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HGPFSQVEDLERVEGITGKQMESFLKANILGLAAGGRCGAS"  Similarity 100.0%; Pred. No. 0;  Similarity 100.0%; Pred. No. 0;  Similarity 100.0%; Pred. No. 0;  Similarity 100.0%; Pred. No. 0;  Similarity 100.0%; Pred. No. 0;  Similarity 100.0%; Pred. No. 0;  GGTCGCTGCTCGCTTGCGGCTAAGCAAGATTGGAACTGACTCGTCCTCCTCGCTTAAGG 33  [[	CGGCCATGGGCCCTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA 483  [
ORIGIN  Query Match Best Local Sim Matches 1458;  Qy 4 GG  Qy 64 GT  Db 100 GG  Qy 124 GG  Oy 224 GG  Oy 280 CT  Ob 3304 TA  Db 340 GG  Oy 364 GT  Db 400 TA  Db GG  Db 400 TA	QY       424         DD       520         QY       484         DD       540         QY       604         DD       760         QY       644         DD       724         DD       724         DD       724         DD       820         QY       784         DD       844         DD       940         QY       904

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                                                        UNH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-remail.inh.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be found
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Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Gaps

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Score 1458; DB 9; Pred. No. 0; 0; Mismatches 0;

99.6%; Scor. 100.0%; Pre

Conservative

Similarity

Query Match Best Local Simi Matches 1458;

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ORIGIN

Length 2117;

63

GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGGCTAAGG

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                     DWA Sequencing by: Genome Sequence Centre, BC. Canada State Canear Agency, Vancouver, BC, Canada Steve Jones, Sarah Barber, Mahel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saedi, JR Sancos, Angelique Schnerch, Ursula Skalska, Bouane Smailus, Jeff Stott, Miranda Teai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: f Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817. Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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1. (bases 1 to 2134)

2. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Wanny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Koung, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A., Schein, J.E., Jones, S.J. and Marza, M.A.
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                                                                                                                                                                  TTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCTCTGTTGAGTACCCCAAAG
                                                                                                                                    CTCAGCCCCTACAGAAGCTAAGCAGCATGACCCGGCCATGCTGGAGCGCCTCCTCAGC
                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
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OGTPILINTPKRERWIJMKTVEEKNIEI ERLKWKGKELEAKVIAQBAPDPREKENTPTI
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EVEDLEQVEGISGKQVESFIKANILISILAASQHSGPS
Series: IRAK Plate: 5 Row: m Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21704181.
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20. .2002
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DEFINITION Sequence 5 from patent US 6387644.  ARCESSION AR210054. VERSION AR210054.1 GI:21512185  KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown.  TITLE AUTHORS BERAUG,C. TITLE JOURNAL PATENT: US 6387644-A 5 14-MAY-2002; FEATURES 1041 / Organism="unknown" / mol_type="unknown" / mol_type="unknown" / mol_type="unknown"	Query Match 70.9%; Score 1038.4; DB 6; Length 1041; Best Local Similarity 99.9%; Pred. No. 1.6e-266; Matches 1039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy         1 ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA 60           Db         1 ATGGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGGCTA 60           Qy         61 AGGGTGGTGGAGCACTTGCGGCCATTTGTGGAACAGCGGGAACAAGTGAAGTGAACTCCCCC 120	Db         6.1 AGGGTGGTGTGCGACTGCGGCATTTGTGGATGGAACAGCGGAGCAAGTGATCGCCCC 120           Qy         12.1 TGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACCAGGAG 180           Db         12.1 TGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAG 180	Oy 181 ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTAT 240  Db 181 ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGGAGACATCTAT 240	Oy 241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTT 300 241 GCAGGTTCAGTGCCACTCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGCGTT 300	Qy         301 GCCTATGGACCCACAGGAGCTGGGAAGACGCACCACAATGCTGGGCAGCCAGAGCAACCT 360           Db         301 GCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCT 360	Oy         361 GGGGTGATCCCGCGGGGTTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGGTGCCGAG         420           Db         361 GGGGTGATCCCGCGGGTTCTCATGGACCTCCTGCAGCTCACAAGGAGGAGGAGGTGCCGAG         420	OY 421 GGCCGGCCATGGGCCCTTTCTGTCATGTCTTACCTAGAGATCTACCGGGGAAAGGTA 480	OY 481 TTAGACCTCCTGGACCCTGGTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAAT 540	Oy 541 ATCCTGATTCCGGGTCTCTCCCAGAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCAC 600 bb. 541 ATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCAC 600	Oy 601 TICCIGCCAGCCAGTGGAATGGGACTGTAGGAGCCACCGGGTCAACCAGGGGTCCTCC 660 b 601 TICCIGCCAGCCAGTGGAATGGGACTGTAGGAGCCACCGGGTCAACCAGGGGTCCTCC 660	Qy         661 CGCAGTCATGCTGCTCCTGGTCAAGGTGGACCAGGGGAAACGTTTGGCCCCATTTCGC         720           Db         661 CGCAGTCATGCTCTGGTCAAGGTCGACCAGCGGGAAACGTTTGGCCCCATTTCGC         720	Oy 721 CAGCGAGAGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACA 780 

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Mus musculus clone RP24-158A6, WORKING DRAFT SEQUENCE, 4 unordered
pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 151041)
                                                                                                                                                                                                                                                                                                                                                                                                                  498 CGGCCATTGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTA
                                                                                             GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGAATATC
                                                                                                                           GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                                                                                                                                                                                          CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                                                                                        CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                                                                                                                                                                                     AGTCATGCTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCCATTTCGCCAG
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AC101919.4 GI:28951338
HTG; HTGS PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
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REFERENCE
AUTHORS
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Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 151041)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, J., Gardyna, S.,

Hall, J., Hortcon, L., Hulme, W., Iliev, I., Johnson, R.,

Lindblad Toh, K., Liu, G., Lui, A., Mabbitt, R., Macclean, C.,

Macdonald, P., Major, J., Manning, J., Marthews, C., McCarthy, M.,

Maddonald, P., Major, J., Manning, J., Marthews, C., McCarthy, M.,

Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Smith, C.,

Spencer, B., Stange-Thomann, N., Schyabon, K., Travers, M.,

Talamas, J., Tesfaye, S., Thedore, J., Topham, K., Travers, M.,

Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

All repeats were identified using RepeatMasker:

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Center, Whitcher of Institute/ MIT Center for Genome Center

Center, Engler of MIT Center for Genome Center of Center for Genome Center of Center for Genome Center of Center of the MIT Center of Center of Center wersion replaced gi:28631351. Center code: WIER
Web site: http://www-seg.wi.mit.edu
Contact: sequence\_Endipsions@genome.wi.mit.edu
Contact: sequence\_Endipsions@genome.wi.mit.edu
Contact: sequence\_Endipsions@genome.wi.mit.edu
Center project name: 11745
Center clone name: 11745
Center clone name: 11745
Center clone name: 158 A. 6
Sequencing vector: Plasmid: n/a; 100% of reads
Sequencing vector: Plasmid: n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150558 bases at least Q40
Consensus quality: 150654 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 151000; agarose-fp
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is 33517: contig of 33517 bp in length 33617: gap of 100 bp 42736: contig of 9119 bp in length

731

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AC101752 164759 bp DNA linear ROD 23-APR-2004
Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
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Biran, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bogualavkiy, L., Boukhgalter, B.,
Anderson, S., Camarata, V., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 164759)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 1, clone RP24-344C18
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 TGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCCATTTCGCCAGCGAGGG
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7 42836: gap of 100 bp
7 84394: contig of 41558 bp in length
5 84494: gap of 100 bp
5 151041: contig of 66547 bp in length.
Location/Qualifiers
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                                                                    1. .151041
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Submitted (17-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, J., Cooke, A., Cooke, P., Corum, B., Chang, J., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., Corum, B., Chang, J., Choepel, Y., Collymore, A., Cooke, R., Cooke, P., Corum, B., Chang, J., Bagoslavki, J., Baro, S., Rerreira, P., FitzGerald, M., Gage, D., Galagan, J., Raro, S., Rerreira, P., FitzGerald, M., Gage, D., Galagan, J., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Johnson, R., Manches, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Macdonald, P., Major, J., Mibova, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Travers, M., Stubbs, M., Talamas, J., Tesfave, S., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schuer, A., Stojanon, J., Zombek, L., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Direct Submission and Zody, M., X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Direct Submission and Solver, Cambridge, MA 02141, USA On Apr 23, 2004 this sequence version replaced gi:45504330.

All repeats were identified using RepeatMasker:
                   Perreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gords, S., Govette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, M., Illiev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Lavine, R., Liu, G., Lamazares, R., Landers T., Lehoczky, J., Levine, R., Liu, G., MacChan, C., MacChan, P., Major, J., Marthews, C., MacCarthy, M., McEwan, P., McTaran, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Shor, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schupback, R., Schupback, S., Schupback, S., Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramann, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Direct, Subnission
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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AUTHORS
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Center: Whitehead Institute/MIT Center for Genome Research
                      Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
Center project Information
Center project name: L1734
Center clone name: 344_C_18
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complement(9800..1
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AC101908
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                                                                                                                                                                                                                                       AGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGGCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 881.8; DB 10;
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1119 ATAATTGTGCCTGTTTGTGGATGAAGAGAAGCGAAGGAGCACCCCTGTGTACGAGC 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999 TCAGTITIGAIGCCTICCAIGGAGAGAGACACTCAGTCAGGACAICTAIGTAGGITTAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 GCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGGACC
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consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                      50.6%; Score 740.6; DB 2; Length 78.2%; Pred. No. 1.1e-186; ive 0; Mismatches 249; Indels
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    .297639
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Best Local Similarity 78.2
Matches 916; Conservative
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73893
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                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Contact: sequence_submissions@broad.mit.edu
------ Project_Information
                                                                                                                      Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 1, clone RP24-275J1
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Center clone name: 275_J_1
       musculus (house mouse)
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Norbu,C., Norman,C.H., O'Connor T., O'Donnall,P., O'Neil,D.,
Ollver,J., Petergon,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Scaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigillo,J., Vassillev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Submitson
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.wahington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (33-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Contact: sequence_submissions@broad.mit.edu
------ Project Information
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Mus musculus chromosome 1, clone RP23-202A19, complete sequence.
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Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Calangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArcellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
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MacCean, C., MacGonald, P., Major, J., Marthis, N., Matthews, C.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                 CAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGCAGTCATGC
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                                                                                                                      581 CAGTAGAAATCGAGTTGTAGGAGCTACTCGCTTAACCAGCGCTCTTGCCGTAGTCATGC
                                                                                                                                                                                                                                                                                                                 672 TGTGCTCCTGGTCAAGGTGGACCAGCGGAACGTTTGGCCCCCATTTCGCCCAGCGAGAGG
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Mus musculus chromosome 1, clone RP23-202A19
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/clone lib="RPCI-23 Female Mouse BAC"
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14. .746
note="single clone coverage"
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4445. 4496

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4445. 4496

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/ rrpt_family="(GAAA)n"

Complement (5434. 5561)

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Complement (6185. 6272)

/ rrpt_family="RMERIS"

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/rpc_family="L1"
Center project name: L18071
Center clone name: 202_A_19
                                                                                              Location/Qualifiers
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102171 TGCCAGCCTGTAGAAATCAAGTTGTAGGAGCTACTCTGCTTAAGCAGTGCTCTTACCATA 102230 101871 101691 101751 101811 101931 8 188 308 128 364 484 604 424 101872 GACTATTGAGGCAGGGAAGACACATATAATACTGGGTAGCCCCATGGGAACAACATGGAG TGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCCCGCA 69 TGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCCTGTGTGCG 129 GGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACGAGGAGTCTCTCAA 101692 addóaitaraaadcidcicircircaadgigdccaccirdaddaaarccrardadaaracraa 189 ATACCAGTITGATGCCTTCTATGGGGAGAGAGTACTCAGCAGGACATCTATGCAGGTTC 101752 ATATCAGTTTAATGTCTTTTATTGAGAGAGAGAGCACTCAGCAGAACATCTAAGTAGGTTC 249 AGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGTGCTTGCCTATGG 101812 AGTACAGCCTATCCTGTGGCACTTGCTGGATGGGCAGATACCAGTGTGCTTACATATGG 309 ACCCACAGGAGGTGGGAAGACGCACACAATGCTGGGCAGCCC----AGAGCAACCTGGGG 365 TGAICCCGCGCGCGCTCTCAIGGACCTCCTGCAGCTCACAAGGGAGGGGGCCCGAGGGCC 425 GGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAG 485 ACCICCIGGACCTICGGAGACCIGGIAAICCGAGAGACTGCCGGGGGAATAICC 545 TGATTTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCC 12; Gaps Length 196674; 48.3%; Score 706.8; DB 10; Length 73.3%; Pred. No. 1.2e-177; ive 0; Mismatches 357; Indels /rpt family="RMER20"
complement (16008 ..16517)
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16809..16866
/rpt\_family="(TG)n"
complement(16922..17052)
/rpt\_family="B4"
/rpt\_family="B4"
/rpt\_family="MLT2B1"
/rpt\_family="MLT2B1" 11555. .12196 /rpt family="Lx2" complement(13221. .13381) /rpt family="B3A" 13437. .13578 rpt\_family="L1\_MM" 1555. .1210f 5222. 15254 -rpt family="AT rich" omplement (15315. 15 /rpt\_family="(GGAA)n" family="B1\_MM" rpt\_family="(A)n" 862. .10368 rpt\_family="Lx2" Best Local Similarity 73.3%; Matches 1013; Conservative repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region 605 102112 Query Match ò ద g ò g g ò 셤 셤 ò 셤 ò 셤 ò ઠે ò ò

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102828 TATATCATTICTIGGGATCTCAGGGGAACAAGAAGGTATACTICTACTGAATACCCCAAA 102887
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102231 -TCATTCAATGCTCTTTATCAAGGTGGATCAGCATGGACATTTGACTCTGTTTCACTAGT 102289
                                                                                                                                                   1323 GCGAGA-GCGGATGGTGCTAATGAAGACAGTAGAAGAAGGACCTAGAGATTGAGAGGC 1381
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Search completed: November 10, 2004, 13:18:11 Job time : 6475.64 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- nucleic search, using sw model OM nucleic

9, 2004, 09:45:10 ; Search time 756.977 Seconds (without alignments) 10152.424 Million cell updates/sec November Run on:

US-10-797-893-7

Title: Perfect score:

1464 1 atgggtogctgtoggctaag......accattgtoccacaatgtga 1464 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4134886 segs, 2624710521 residues Searched:

8269772

seq length: 0 seq length: 200000000 Minimum DB R Maximum DB R

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

N\_Geneseq\_23Sep04:\* .: geneseqn1980s:\* :: geneseqn1990s:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2003as:\* geneseqn2001as:\* geneseqn2002bs:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:\* geneseqn2003ds:\*

geneseqn2004s:

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Result		Query				
No.	Score	Match	Match Length DB	8	QI QI	Description
-	1464	100.0	1464	2	ADC23343	Adc23343 DNA encod
7	1464	100.0	1464	12	ADQ60233	
m	1461	99.8	1538	10	ADC23339	Adc23339 DNA encod
4	1461	99.8	1538	12	ADQ60229	
S	1458	9.66	2097	12	ADQ09241	Add09241 Human KNS
9	1447	98.8	2099	10	ADK40995	Adk40995 Novel hum
7	1443.2	98.6	2104	٣	AAF15853	Aaf15853 Human pro
60	1038.4	70.9	1041	10	ADC23341	Adc23341 DNA encod
6	1038.4	70.9	1041	12	ADQ60231	Add60231 Human mic
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11	1035.4	70.7	1115	12	ADQ60227	Adq60227 Human mic
12	480	32.8	491	9	ABK70260	Abk70260 Human lun
13	376.4	25.7	386	4	AAS38879	Aas38879 Novel hum
14	265	18.1	464	σ	ACH44493	Ach44493 Human foe
15	233.2	15.9	531	12	ACH77408	Ach77408 Human gen
16	230.4	15.7	232	12	ACH91108	Ach91108 Human gen
17	185.6	12.7	2095	11	ADM01564	Adm01564 Human CDN
18	185.6	12.7	3624	12	ADO44181	Ado44181 DNA encod
19	156.8	10.7	3374	10	ADJ95073	Adj95073 Novel NOV
20	154.8	10.6	2375	ω	ABX34596	Abx34596 Human mdd
21	138.6	9.5	4108	9	ABA94614	Aba94614 Human kin

## ALIGNMENTS

RESULT 1

DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 7) ADC23343 standard; DNA; 1464 BP. (first entry) 18-DEC-2003 ADC23343; ADC23343 

human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.

Homo sapiens

/product= "KID protein" Location/Qualifiers æ 1. .1464 /\*tag= a

US6387644-B1.

14-MAY-2002.

28-NOV-2000; 2000US-00724224.

20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292.

(CYTO-) CYTOKINETICS INC.

Beraud C;

WPI; 2003-706919/67. P-PSDB; ADC23344.

Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.

Disclosure; SEQ ID NO 7; 26pp; English

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1201 AAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCCGGCCATGCTGGAGCGCCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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                                                                                                CCTGAGGAAGAAGAGTTTGGGAGCCCTGAGCCCCATGGCAGCTCCAGCCTCTGCCTCCCAG
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                                                                                                                                                ATTGCCCCTGAGAGGCTTCTACCTAGACACACTCCGCACTCAACTTTGCTGCCAGG
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1. .1464
A-taga microtubule motor protein /product = "Human microtubule motor protein"
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   This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP to phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, testenosis, cardiac hypertrophy, immune disorders and inflammation. This polymucleotide sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Matches 1464; Conservative
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New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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                                                20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                 06-MAR-2002; 2002US-00093317
                                                                                  (CYTO-) CYTOKINETICS INC.
                                                                                                                    WPI; 2004-532491/51.
P-PSDB; ADQ60234.
US6762043-B1
                13-JUL-2004
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421 481 481 541 541 361 421 1021 1201 1201 601 601 841 901 1081 1081 1141 1141 1261 1261 1321 1321 1381 1381 661 661 721 721 781 781 841 901 961 요 ઠે g ઠે g 셤 엄 g ò ŝ ઠે ò a ò 요 ઠે ద ò a à g ò 셤 ò 8 셤 셤 셤 ઠ ò ò g ð ò cacids encoding them. The invention microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing. For Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target proteins, methods to identify candidate agents that bind to a target or protein or act as a modulator of the binding characteristics or concern, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular complexity of modulators of motor proteins useful for treating callular complexity immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune disorders as associated with KID and for inhibiting KID and for treating autoimmune disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and and poplasty. This sequence represents DNA encoding a human microtubule company and contor protein of the invention. invention relates to human microtubule motor proteins and the nucleic 240 360 AGGGTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCC 120 120 TGTGTGCGGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAACCACCAGGAG 180 180 240 300 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCCAGAATGCCAGTGTGCTT 300 9 9 ATGGTCGCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA ATGGCTCCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTA ACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTAT GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTT AGGGTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCC ACTUTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTAT GCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCT Gaps 241 241 301 301

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1020 1020 1080 1080 1140 1200 1200 1260 1260 1320 1320 1380 1440 1140 1380 480 480 540 909 540 600 9 420 660 720 720 780 780 840 840 900 900 960 960 361 GGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTACAAGGAGGAGGAGGAGGAGCTGCCGAG GGGTGATCCCGCGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGAGGTGCCGAG TTAGACCTCCTGGACCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAAT ATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGGTGATTTTGAGCGGCAC GGCAAAGTGGTAGATGGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG GGCCGCCCATGCGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTA Tradaccriccrideaccriccriceseagaccrigeraarcceagaagacricceggggaar Trecreecedecagresaaresaacrerassasececesereasecaseceree CGCAGTCATGCTGTCTCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGC CAGCGAGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACA GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG GCCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG CTCACTCGCCTATTGCAGGACTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGG 961 ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGACTCTCCGCACTCAACTTTGCTGCCAGG TCCAAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGA 1021 rccaaggaggrgarcaarcggccrrrraccaargagagccrgcagccrcargccrrrgga CCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGCCCGAGGC CCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACAGAGGCAAAGAGAGCCCGAGGC CCTGAGGAAGAGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCAG CCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCTCCCAG AAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGCGCCTCCTC AGCTTGGACCGTCTGCCTTGCCTCCCAGGGGAGCCAGGGGCCCCTCTGTTGAGTACCCCA AAGCGAGGCGCATGCTAATGAAGACAGTAGAAGAGGAGCCTAGAGATTGAGAGG AAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAGAAGGACCTAGAGAGATTGAGAGG CTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTTGGCCCCAGAAGGCTGAGGAAAAG AGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCTC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 3) encoding a full length
                                                                                                                                                                                                                                                                                                                                                                                                      /transl except= (pos: 4. .5; aa: Pro)
/note= "This codon has an apparent 1 nucleotide deletion
that alters the reading frame"
                                                                                                                                                                                                DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 3)
                                                                                                                                                                                                                             human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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99.8%; Score 1461; DB 10; Length 1538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 0; Indels 0;
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/*tag= a
/product= "KID protein"
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           1441 GAGAACCATTGTCCCACAATGTGA 1464
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GAGAACCATTGTCCCACAATGTGA
                                                                                                         ВВ
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20-JUN-2000; 2000US-00597292.
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                                                                                                           ADC23339 standard; DNA; 1538
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                                                                                                                                                                        (first entry)
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P-PSDB; ADC23340.
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         78 GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCGACCTCCAGCTCGGCGTAAGG
                                                                                                                        GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC
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                                   GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGAGCAAGTGATCCCCCCTGT
                                              124 GTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like bNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microtubule motor protein DNA #2.
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activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target cancer, hyperplasias, restencesis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restences, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune associated with KID and for inhibiting KID and for treating autoimmune associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and comproplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention. Note: The specification states that this expense the protein featured as SEQ ID NO:4, but this does not
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Human KNSL4 encoding cDNA SEQ ID NO:426. ADQ09241 standard; cDNA; 2097 (first entry) 23-SEP-2004 ADQ09241; 

thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; anglogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antianglogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;

WO2004055050-A2 Homo sapiens

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The present invention describes a method for modulating the expression of a thantos (dasth)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a mucleic acid, and so enhancing or repression the expression of the THAP responsive gene. Also described (1) a method of modulating the expression of a gene responsive to a THAP responsive complex; (2) a pharmaceutical composition comprising a THAP responsive comprising a transcription factor decoy described above, (5) methods of the polypeptide or its piological fragment, or a mucleic acid and a THAP-family polypeptide or its piological fragment; (3) a transcription factor decoy described above, (5) methods or its piological fragment; or a mucleic acid and a THAP-family polypeptide or its piological fragment or a mucleic acid and a THAP-family polypeptide or its piological fragment; (6) a weetor packaging cell line complex; (6) a vector packaging cell line complex; (7) a method of constructing a cell which expresses a combinant THAP-family polypeptide; (9) a method of ameliorating recombinant THAP-family polypeptide; (9) a method of ameliorating combinant into the nucleus; (10) methods for reducing the symptoms associated with a condition mediated by a THAP/chemokine complex; (9) methods of identifying a test compound that modulates transcription complex; (10) methods for reducing the symptoms associated with a condition mediated by a THAP/chemokine or an insufficient apoptosis; cardiovascular disease and meurodegenerative or insufficient apoptosis; cardiovascular disease and meurodegenerative or insufficient apoptosis; cardiovascular disease and meurodegenerative or insufficient apoptosis; cardiovascular disease and meurodegenerative comprising a THAP-family polypeptide in an individual; or comprising a THAP responsive promoter; (12) a genetically engineered by a THAP-family polypeptide or a THAP-family polypeptide in an individual; (11) a mentod or comprising a THAP r
                                                                                                                                                                                                                                                                                                                                                   responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
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                                                                                                                                                                                                                                                                                                                                  expression of a Thanatos (death) - Associated Protein (THAP)
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03-JUL-2003;
                   01-JUL-2004
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Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other;

Gaps ; 0 DB 12; Length 2097; Indels ; 99.6%; Score 1458; D 100.0%; Pred. No. 0; ive 0; Mismatches Query Match Best Local Similarity 100. Matches 1458; Conservative

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Qy         1180 GTTAAGCTGTCTCAGAAGAATTGCTTGGTCCACCAGAGGCAAAGAAGAGGCCCGAGGCCCT         1139           Db         1180 GTTAAGCTGTCTCAGAAATTGCTTGGTCCACCAGAGGCCCAAAGAGGCCCGAGGCCCT         1239           Qy         1144 GAGGAAGAGAATTGGGAGCCTGAGCCCATGGCTCCAGCTCTCCCTCC	RESULT 6 ADX40995 ID ADX40995 standard; DNA; 2099 BP. XX AC ADX40995; XX DE G-MAY-2004 (first entry) XX DE Novel human kinase gene #15. XX MY Cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; XM Alzhaimez, disease; parkinsonian; virucide; antibacterial; fungicide ophthalmological; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Alzhaimez's disease; parkinson's disease; multiple calcerosis; XM Mycoloric disorder; cognition disorder; hypotension; hypertension; XM Mycolosofic disorder; organ transplant rejection; enzyme; gene; ds. XX XX XX XX XX XX XX XX XX XX XX XX XX	
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The mucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprise an aturally occurring kinase polypeptide; (d) encodes the encodes a naturally occurring kinase polypeptide; (d) encodes the conspected in (a), except that it lacks one or more, but not all, of an N-terminal domain, C-terminal catalytic domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are conscretably cancers, cardiovascular disease, brain or neuronal or peripheral nervous system, Alzhaimer's diseases of the central or peripheral nervous system, Alzhaimer's diseases of the central or peripheral nervous system, Alzhaimer's diseases of conterior, infections, infections caused by prions, infections caused by kinds, ocular diseases, migraines, pain, excert in infections, infections caused by prions, infections caused by kinds, ocular diseases, migraines, pain, excert in the contern of the invention, general disorders, diseases, migraines, pain, expected disorders, diseases, migraines, pain, exception. This sequence corresponds to the DNA encoding one of the cyx, in the content of the invention. 

Sequence 2099 BP; 484 A; 592 C; 628 G; 395 T; 0 U; 0 Other;

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760 280 340 400 363 460 423 520 483 580 543 603 700 663 243 303 123 220 GTGGCTGTGCGACTGCGGCCATTTGTGGATGAACAGCGGGAGCAAGTGATCCCCCTGT TATGGACCCACAGGAGCTGGGAAGACGCACACACATGCTGGGCAGCCCAGAGCAACCTGGG GTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGGCCGAGGGCCACAAGGGAGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGAGGAGGAGGCGCGAGGC CGGCCATGGGCCCTTTCTGTCACCATGTCTACCTAGAGATCTACCAGGAGAAGGTATTA GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC CTGATTCCGGGTCTCTCCCGGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC creatricessiticesaagecearcagragemengergartrigasgecere CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC CTCAAATACCAGTTTGATGCCTTCTATGGGGAGGAGGAGTACTCAGCAGGACATCTATGCA GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGTTGCC GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGTTGCC GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG Gaps ... T Length 2099; Indels Query Match
98.8%; Score 1447; DB 10;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1458; Conservative 0; Mismatches 0; 484 544 701 4 101 64 191 124 221 184 281 244 341 304 401 364 461 424 521 641 8 d à à 셤 ò g à g 8 g ò g ò 셤 ò 셤 ò 유

1420 1323 1383 TAAGACGAAAAAAAAAAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTGAGGAAAAGGA 1442 1023 Human, prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunocdulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; 1000 880 843 940 963 783 CGAGAGCGGATGCTAATGAAGACAGTAGAAGAGAAGGACCTAG-AGATTGAGAGGCT CTCAGCCCCCTACAGAAGCTAAAGCAGCATGACCAGCCATGCTGGAGCGCCTCAGG 1264 TTGGACCGTCTGCTTGCCTCCCAGGGGGGCCAGGGGCCCCTCTGTTGAGTACCCCAAAG 1421 CGAGAGCGGATGCTGCTAATGAAGACAGTAGAAGAAGAACGAGTAGATTGAGAGGCT AACAAGGGCCTTCGGCTAAAAGAGAGGGGATCAACACCCTCCTGTTTGTCCTGGGC AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTC ACTOGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCAGTATCCTTATTGCCAACATT GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCCACTCAACTTTGCTGCCAGGTCC AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGACCT GTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGCCCGAGGCCCT GAGGAAGAGGAGTTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCTCCCAGAAA CTCAGCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGCGCCTCCTCAGC CGAGAGAGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACGGGCGCACAGGC Human prostate cancer antigen nucleotide sequence SEQ ID NO:288. 1443 GAACCATTGTCCCACAATG 1461 BP AAF15853 standard; cDNA; 2104 GAACCATTGTCCCACAATG entry) (first 13-MAR-2001 904 1001 1024 1121 1084 1144 1204 1301 1324 1541 AAF15853; 844 964 784 761 724 RESULT 7 g g 셤 8 8 요 ò 셤 ઠે g ò 엄 ò 요 ò 셤 ò g ઠ ઠે g ò ò δ ద ò

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Pred. No. 3.1e-278;
0; Mismatches 1; II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPases activity, a method so festing for ATPases activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders as associated with KID and for inhibiting KID and for treating autoimmune disorders such inflammation, for treating disorders as associated with KID and for inhibiting KID and for treating disorders proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and angloplasty. In sequence represents DNA encoding a human microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                           Human; microtubule motor protein; gene; de; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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Pred. No. 3.1e-278;
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Human microtubule motor protein DNA #3
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                                                                                                                                                                                                                                       /transl_except= (pos: 1. .5; aa: Met) /note= "This codon has an apparent 2 nucleotide insertion that alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
     DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1035.4; DB 10; Length 1115;
Pred. No. 2.2e-277;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1115 BP; 241 A; 318 C; 333 G; 223 T; 0 U; 0 Other;
                                                                                                                                                                                                           /*tag= a
/product= "KID protein"
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                                                                                                                                                                       Location/Qualifiers
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Best Local Similarity 99.9%;
Matches 1036; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1999; 99US-00295612
20-JUN-2000; 2000US-00597292
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GTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGAGACT
                                                                    GTGATCCCGCGGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGAGGCTGCCGAGGGC
                                           CICAAATACCAGTTTGATGCCTTCTATGGGGGGGGGGGTGTACTCAGCAGGACATCTATGCA
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GGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAAATGCCAGTGTGCTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a methods of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenoois, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune disorders and inflammatory bowel disease and proliferation induced after medical procedures including surgery and anglophasty. This sequence represents DNA encoding a human microtubile motor protein of the invention of the invention when the contents and inflammatory bowel disease and propolatory and the anglophasty. This sequence represents DNA encoding a human microtubile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        motor protein of the invention. Note: The specification states that this sequence encodes the protein featured as SEQ ID NO:2, but this does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
               Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1115 BP; 241 A; 318 C; 333 G; 223 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                      20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                       06-MAR-2002; 2002US-00093317
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOKINETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.9
Matches 1036, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             appear to be the case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-532491/51
                                                                                                                                                                                                          US6762043-B1
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                       13-JUL-2004
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The invention relates to new polymucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39333 represent novel human diagnostic and therapeutic coding sequences of the invention
                                                                                                                                                                                                                                                               1356 AGAGAAGGACCTAGAGATTGAGAGGCTTAAGACGAAAGCAAAAAGAACTGGAGGCCAAGAT 1415
                                                                                                             1236 CCCGGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCA 1295
                                                                                                                                  300 CCCGGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGAGCGCA 359
                                                                                                                                                                                                                      360 GGGGCCCCTCTCTTTGATACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGT 419
                                                                                                                                                                                                                                                                                       180 ACCAGAGGCAAAGAGAGCCCCGAGGCCCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynuclectides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
                                                                                                                                                                                       1296 GGGGGCCCCTCTGTTGAGTACCCCAAAGCGAGGGGGATGGTGGTGATGAAGACAGTAGA
                                                          240 GGCAGCTCCAGCCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGA
                                         GGCAGCTCCAGCCTCCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garcia PD, Sudduth-Klinger J,
Pot D, Kassam A, Lamson G;
I, Drmanc S, Labat I;
nes WL, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 118 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic and therapeutic gene #1937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.7%; Score 376.4; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Escobedo J, Innis MA, Garcia I
Randazzo F, Kennedy GC, Pot D,
Crkvenjakov R, Dickson M, Drmana
D, Kita D, Garcia V, Jones WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1080; 1193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS38879 standard; cDNA; 386 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 386 BP; 105 A; 102
                                                                                                                                                                                                                                                                                                                                              1416 GTTGGCCCAGAA 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 480 Grredecceada 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200166753-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams LT,
Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS38879;
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                                            1176
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polymucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded to polypeptides. Also included are an expression vector comprising the polymucleotide operably linked to an expression vector of; an isolated cell transformed or transfected with an expression control sequence; a host controlectide operably linked to an expression vector of; an isolated cell transformed or transfected with an expression vector of; an isolated controlectide is method for detecting the presence of a cancer in a patient of a fusion protein comprising at least the polympetide; an operately of component conditions; a method for stimulating and/or expanding T cells stringent conditions; an isolated T cell population of arriers and immunostimulants, and a second component selected from the polymucleotides, proteins, antibodies, fusion component selected from the polymucleotides, proteins, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polymetion reagent consisting of arriers and immune response or treating to proteins, T cell populations and antigen presenting cells expressing the compositing at least one of the oligonucleotide of, or an antibody and a detection reagent consisting of a reporter group. The polymeptides are useful as vaccines for the treatment or prevention of polymucleotides are useful as vaccines for the treatment or prevention of ung cancer, and for diagnosis and monitoring of such cancer. The polymucleotides may be used as probes or primers for mucleotides con an integer presenting cells con the public transfer or an integer or treating colling the preparesion of tunour polypeptides or an antibody and a colling thing expression of tunour polypeptides or an expect or tunour polypeptide and antigen presenting cells con the preparation of the oligonucleotides may be used as probes or primers for mucleic acid for the preparati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1055
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                                                                                                                                                                                                                                                                                                                                  New tumor lung proteins and nucleic acids encoding the proteins, useful as vaccines and for treating, preventing, diagnosing or monitoring lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  936 AGCCCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCGCACTCAACTTTGCTGCCAAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 480; DB 6; Length 49
Pred. No. 5.3e-123;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 144; 189pp; English
                                                                                                                                                                                                                                                               Lodes MJ
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                                                                                                                                              22-SEP-2000; 2000US-0234837P.
10-OCT-2000; 2000US-0239440P.
29-JUN-2001; 2001US-0301928P.
                                                                                                         20-SEP-2001; 2001WO-US042232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.8
Matches 491, Conservative
                                                                                                                                                                                                                                                             Benson DR, Mohamath R,
                                                                                                                                                                                                                                                                                                 WPI; 2002-372001/40:
                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                       WO200224057-A2
                                                                        28-MAR-2002.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 88; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide comprising any one of
                                                                  9
                                      CCTTGGGACCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGA
                                                       CCCGAGGCCCTGAGGAAGAGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTG
                                                                                                        61 CCCGAGGCCCTGAGGAAGAAGAAGAATTGGGAAGCCCTGAGGCCCATGGCAAGCTCCAGCCTCTG
                                                                                                                                          CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGC
                                                                                                                                                                                                                    181 GCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCCTCTGTTGA
                                                                                                                                                                                                                                             GTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGGACCTAGAGA
                                                                                                                                                                                                                                                                       GTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGAAGGACCTAGAGA
                                                                                                                                                                                                                                                                                                TTGAGAGGCTTAAGACGAAGAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCTG
                                                                                                                                                                                                                                                                                                                         TTGAGAGGCTTAAGACGAAGAAGAACTGGAGGCCCAAGATGTTGGCCCCAGAAGGCTG
                                                                                                                                                                  121 CCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGACCCGGCCATGCTGGAGC
                 Gaps
                 ;
                                                                                                                                                                                            GCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones LW;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dickson MC,
 Pred. No. 3.2e-94;
); Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                AGGAAAAGGAGAACCATTGTCCCACA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 31705; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                 AGGAAAAGGAGAACCATTGTCCCACA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal brain cDNA #5218
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH44493 standard; cDNA; 464
  98.48;
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              380; Conservative
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STACHE-CRAIN B
DICKSON M C.
JONES L W.
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Best Local Similarity
Matches 380; Conserv
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(LABA/)
(STAC/)
(DICK/)
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determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one the 38043 isolated cDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. The sequence contained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GCGGGCCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACTCT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                             Length 464;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
18.1%; Score 265; DB 9; Length 46
Best Local Similarity 77.6%; Pred. No. 3.5e-63;
Matches 333; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 464 BP; 96 A; 136 C; 131 G; 96 T; 0 U; 5 Other;
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03-APR-2002; 2002US-00029386.
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                                                                                                          (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
16-OCT-2003.
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Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 15; SEQ ID NO 10603; 80pp; English.

The invention relates to a mucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide superences in the specification, or their complements or fragments, and sequences in the specification. The probe is a single exon probe that this defined in the specification. The probe is a single exon probe that this fartingency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-defensable set of single exon nucleic acid probes for measuring human gene expression, comprising a plurality of single exon nucleic acid molecule or and addressably isolatable or amplifiable from the plurality), a single ox measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon nicroarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid of any of the above-mentioned amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, can calso measure gene expression, a method of provading exon probes or solution and an expression data by subscription, and a computer-readable catorage medulum which contains a database having a plurality of records catorage medulum which contains a database having a plurality of records catorage medulum which contains a database having a plurality of cords catorage medulum which contains a database having a plurality of seconds cited above. The probes methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying cated above. The probes are used in identifying and contains a database having a plurality of cords in addition, the probes are used in identifying and contains a laterations in the genomic locus that included second or in expressing the ORF-encoded peptide. The sequence are setul in an human sin the form part of the printed specification, but was obtained seqdata.uspto.gov/sequence.html?DocID=20030194704 directly from USPTO

Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;

743 93 34 ccaegreeaccaeceaacerrreecccarrreeccaecaagagaaaacreracr 684 CAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGGGGAAAAACTCTACCT Gaps . 0 DB 12; Length 531; 3; Indels Query Match 15.9%; Score 233.2; DB 1; Best Local Similarity 98.7%; Pred. No. 2.6e-54; Matches 235; Conservative 0; Mismatches 3; Š 유 AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA

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154 AGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 213 214 TCAGGGCCTCCCTCGTGTACCTTATCGGGAAGCTCACTCGCCTATTGCAGGCC 271 864 TCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGAC 921 음 à g

Search completed: November 10, 2004, 06:58:00 Job time: 760.977 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                    - protein search, using sw model
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5, 2004, 18:34:12 ; Search time 75.9417 Seconds (without alignments) 1747.786 Million cell updates/sec

1 MAAGGSTQQRRREMAAASAA......FYLDTVSALNFAARSKEVIN 370 US-10-797-893-2 1878 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2003ss: geneseqp2003bs: geneseqp2003bs: A\_Geneseq\_23Sep04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result		Query				
No.	Score	Match	Length	BB	ច	Description
+	1878	100.0	370	7	ADC23338	Adc23338 Human kin
7	1878	100.0	370	œ	ADQ60228	Adq60228 Human mic
m	1878	100.0	490	7	ADK40973	
4	1878	100.0	665	œ	ADQ09240	_
S	1873	99.7	512	7	ADC23340	O Human
9	1873	99.7	512	œ	ADQ60230	Human
7	1763	93.9	346	7	ADC23342	٠.
60	1763	93.9	346	œ	ADQ60232	Adq60232 Human mic
σ	1763	93.9	460	m	AAB56650	0
10	1763	93.9	487	7	ADC23344	
11	1763	93.9	487	8	ADQ60234	Human
12	559.5	29.8	784	4	ABB71112	
13	559	29.8		7	ADM04007	Adm04007 Human pro
14	559	29.8		00	AD044167	Ado44167 Structura
15	552.5	29.4	357	ß	AAU76958	Aau76958 Novel hum
16	552.5	29.4	898	4	ABU53123	Abu53123 Intracell
17	552.5	29.4	898	ഹ	AAU76957	Aau76957 Novel hum
18	552.5	29.4	868	7	ADC31082	2 Human
19	552.5	29.4	868	7	ADI15915	Adil5915 Human PP
20	551.5	29.4	603	9	ABU11606	Abull606 Human MDD
21	549	29.5	905	S	AAU76967	Aau76967 Novel hum
22	541	28.8	408	œ	ADN40550	0
23	541	28.8	408	60	ADN4 0554	Adn40554 Candida a
24	541	28.8	972	œ	ADN40548	Adn40548 Candida a
25	541	28.8	974	œ	ADN4 0552	Adn40552 Candida a

This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor

Claim 1; SEQ ID NO 2; 26pp; English.

Abb65183 Drosophil	Abb07412 Amino aci	Abg72053 Human HsK		Abg72052 Human kin		Aae14402 Human HsK	Aau79592 Human HsK	Human	Human	Aau79590 Human kin	Abr48222 Human bla	Adb80468 Ovarian c	Adc35116 Human bre	Adl83290 Human PRO	Adg20128 Human sof	Adq09226 Human KNS	Human	Human N	Adj95078 Novel NOV
ABB65183	ABB07412	ABG72053	ABB07410	ABG72052	AAE14401	AAE14402	AAU79592	ADC31540	AAE14400	AAU79590	ABR48222	ADB80468	ADC35116	. ADL83290	ADQ20128	ADQ09226	AAU19569	ABP51294	ADJ95078
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28.5	28.1	28.1	28.1	28.1	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	27.9
535.5	528	528	528	528	526	526	526	526	526	526	526	526	526	526	526	526	525.5	525.5	523.5
26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                               Human kinesin-like DNA binding protein (KID) (SeqID 2).
                                                                                                                                                                                                                /note= "Encoded by ATGCA"
                                                                                                                                                                                         Location/Qualifiers
           ADC23338 standard; protein; 370 AA.
                                                                                                                                                                                                                                                                                      28-NOV-2000; 2000US-00724224.
                                                                                                                                                                                                                                                                                                            20-APR-1999; 99US-00295612
20-JUN-2000; 2000US-00597292.
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                (CYTO-) CYTOKINETICS INC.
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N-PSDB; ADC23337.
                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                  Homo sapiens:
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                                 ADC23338;
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ADC23338
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120
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domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 2) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplaaia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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                                                                                                                                                                                                                                                                                          SDPPCVRGMDSCSLEIANWRNHQETLKXQFDAFYGERSTQQDIYAGSVQFILRHLLEGGN
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                                                                                                                                                                           Length 370;
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                                                                                                                                                                           100.0%; Score 1878; DB 7;
100.0%; Pred. No. 3.8e-182;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such so cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor protein useful for treating callular corpliferation disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and cases associated with KID and for inhibiting KID and for treating succise of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
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                                                                              New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1878; DB 8;
100.0%; Pred. No. 3.8e-182;
iive 0; Mismatches 0;
                                                                                                                                                                               claim 1; SEQ ID NO 2; 26pp; English
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Matches 370; Conservative
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SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN

SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN

61 69 121 129 181 181

**ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIY** 

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                                                                                                                       antiparkinsonian; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypotension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 80; 491pp; English.
                                                                               Novel human kinase protein #80.
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                          06-MAY-2004
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ADK40973;
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300
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                                                              LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360
                                                                            Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for modulating the expression of a thantoos (death) -associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing
                                                                                                                                                                                                                                                                                                                                                                             THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                        QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS
 QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS
                                                                                                                                                                                                                                                                                                                                                               thanatos-associated protein; THAP; THAP responsive gene; THAP family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clouaire T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 47; SEQ ID NO 425; 612pp; English.
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                                                                                                                                                                                                                                     ADQ09240 standard; protein; 665 AA
                                                                                                                                                                                                                                                                                                                                  Human KNSL4 protein SEQ ID NO:425.
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                                                                                                                         FAARSKEVIN 370
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Length 490;

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Best Local Similarity 100. Matches 370; Conservative

Query Match

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the expression of the THAP responsive gene. Also described: (1) a method complexity (2) a pharmaceutical composition comprising a redulating the expression of a gene responsive to a THAP responsive clement in a pharmaceutical composition comprising a central composition comprising a cell meant in a pharmaceutical composition factor decoy comprising a transcription factor decoy described above; (5) methods of comprising a transcription between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment; (7) a method of constructing. CC c a nucleic acid encoding a THAP-family polypeptide or its biological crecombinant THAP-family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP-family polypeptide or its biological crecombinant THAP-family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP-family polypeptide in a nindividual; or a transcription at a THAP responsive element or that modulates the transcription associated with a condition selected from excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative corporated with a condition selected from excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative comprising a THAP-family polypeptide in an individual; (11) a cartivity of a chemokine or a THAP-family polypeptide in an individual; (11) a mediated by a THAP-family polypeptide in an individual; (11) a cartivity or and product; (12) a genetically in the responsive promoter comprising a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription comprising a nucleic acid comprising a THAP responsive and osteopathic acid comprising a nucleic acid comprising a the vector described above or that expresses a a THAP-family confused modulating the expression of anther accomposition has antiangl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the
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ö ORSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300 QRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTS 300 LFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALN 360 SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQN 120 121 ASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLBIY 180 QEKVLDILLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLN 240 1 MAAGGSTQORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA 60 61 SDPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILKHLLEGQN 1 MAAGGSTOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGA Gaps ö 100.0%; Score 1878; DB 8; Length 665; 100.0%; Pred. No. 9.5e-182; ive 0; Mismatches 0; Indels 0 Query Match Best Local Similarity 100. Matches 370; Conservative FAARSKEVIN 370 121 181 181 241 241 301 61 셤 g ò g ð g ò g δ à

Sequence 665 AA;

Internation disorders. Specifically, it refers to candidate agents that proliferation disorders. Specifically, it refers to candidate agents that dear capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using or phosphate. Furthermore readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This

This invention relates to a novel method for high throughput

restenosis, cardiac hypertrophy, immune disorders and inflammation. Tropolypeptide sequence is human KID protein (SeqID 4) of the invention.

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99.7%; Score 1873; DB 7; llarity 100.0%; Pred. No. 2e-181; Conservative 0; Mismatches 0

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Sequence 512 AA;

DB 7; Length 512; Indels 61 62 DPPCVRGMDSCSLBIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGGNA 121

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AAGGSTQQRRREMAAASAAA1SGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS 2 AAGGSTOORRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS

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human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                 Human kinesin-like DNA binding protein (KID) (SeqID 4).
                                                                                                                                                                                                                                   /note= "Encoded by CA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4; 26pp; English.
                                                                                                                                                                                                               Location/Qualifiers
                                                    ADC23340 standard; protein; 512 AA.
                                                                                                                                                                                                                                                                                                  28-NOV-2000; 2000US-00724224.
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20-JUN-2000; 2000US-00597292.
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361 FAARSKEVIN 370
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Best Local Similarity
                                                                                                                                         Sequence 512 AA;
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                                           SVLAYGPTGAGKTHTWLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ 182
                                                                     241
                                                                              RSSRSHAVILIVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSL 301
                                                                                                                             DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
                                                                                                                                                            FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 361
                                                                                                                                                                                                                                                                                                                                                                                Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                     SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ
                                                                 EKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQ
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                                                                                                                                                                                                                                                                                                                                                           Human microtubule motor protein #2.
                                                                                                                                                                                                                                                                                        ADQ60230 standard; protein; 512
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulacors of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthatis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasity. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEO ID NO:3, but this does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAGGSTQQRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinesin-like DNA binding protein (KID) (SeqID 6).
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60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1873;
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20-APR-1999;
                                                                                                                               20-JUN-2000;
28-NOV-2000;
           Homo sapiens
                                    US6762043-B1
                                                             13-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                           in surventure trades to a mover merical tradement of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VIPRALMDLLÓLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, microtubule motor protein, cellular proliferation disorder, cancer; hyperplasia; restenosis, cardiac hypertrophy, immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                        Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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                                                                                                                                                                                     This invention relates to a novel method for high throughput
                                                                                                                                                                                                                                                                                                                                                                                                    93.9%; Score 1763; DB 7; Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 1.8e-170; ive 0; Mismatches 0;
                                                                                                                                                            Claim 1; SEQ ID NO 6; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microtubule motor protein #3.
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 345; Conservative
(CYTO-) CYTOKINETICS INC
                                                     WPI; 2003-706919/67.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 346 AA;
                                                                N-PSDB; ADC23341
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for addulators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for creating for modulators of motor proteins useful for treating disorders and inflammation fiscates and inflammation for treating disorders and inflammation for treating disorders and inflammation, for treating disorders and inflammation, for treating disorders and inflammation, for treating disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders and inflammatory bowel disease and proliferation induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and and proliferation induced after medical procedures including surgery and contraction and an analysis and the medical procedures including surgery and and proliferation induced after medical procedures including surgery and and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis and an analysis an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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93.9%; Score 1763; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.8e-170;
Matches 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 6; 26pp; English
                                                                                       99US-00295612.
                                                                                                                           2000US-00597292.
06-MAR-2002; 2002US-00093317.
                                                                                                                                                                                                                                                                (CYTO-) CYTOKINETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-532491/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-532491/
N-PSDB; ADQ60231.
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ETLKYQFDAFYGEXSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQ 121

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PGVI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRG

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                                                                                                                                                                                       neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antibrective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP15566 to AAP16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                issociated gene sequences, referred to as prostate cancer for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                              cancer antigen; detection; diagnosis;
                                                                                                                                                     Human prostate cancer antigen protein sequence SEQ ID NO:1228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 460;
TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
              TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1763; DB 3;
Pred. No. 2.8e-170;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11, Page 1649-1651, 2338pp; English.
                                                                                AAB56650 standard; protein; 460 AA
                                                                                                                                                                              Human; prostate cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.4%;
Matches 345; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US005988
                                                                                                                                                                                                                                                                                                                                                            99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer associated antigens, useful for treatm such as prostate cancer.
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-587513/55.
N-PSDB; AAF15853.
                                                                                                                                                                                                                                                                                                                                                                                             (ROSE/) ROSEN C A.
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 8) of the invention.
                                                                                              263
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                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                    242 ROREGKLYLIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNGGLPRVPYRDS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
NILIPGLSOKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF
                                                                                                                                                                                                                                      ROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDS
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protein for treating cellular proliferation disorders by adding
candidate agent to a mixture of the target protein that
directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                                                                                                                                                                         KLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                                                                                                                                                                 302 KLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human kinesin-like DNA binding protein (KID) (SeqID 8).
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20-JUN-2000; 2000US-00597292.
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N-PSDB; ADC23343.
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GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ

24 GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ

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84 ETLKYOPDAFYGERSTOODIYAGSVOPILRHLLEGONASVLAYGFTGAGKTHTMLGSFEO

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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                  Sequence 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; dev
pharmaceutical.
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                                                                                                REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 325
                                                                                                                                                                                                       Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restencis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                    82
                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                                      LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                        VIPRALMDLLQLTREBGAEGRPWALSVTMSYLBIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                           LI PGLSQKPI SSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                      26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                               2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLBIANWRNHQET
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                  Length 487;
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                  Score 1763; DB 7; I
Pred. No. 3.1e-170;
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             Claim 1; SEQ ID NO 8; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                 Human microtubule motor protein #4.
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2000US-00597292.
2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                (first entry)
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                                      Conservative
                         al Similarity
345; Conservat
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   Sequence 487 AA;
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20-JUN-2000;
28-NOV-2000;
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acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target cancer, hyperplasias, restencing callular proliferation disorders such as cancer, hyperplasias, restencist, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating callular proliferation disorders such as cancer, hyperplasias, restences; chypertrophy, immune disorders and inflammation, for treating autoimmune associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammaticy howel disease and chimibiting KID and for treating autoimmune casociated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammaticy bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein
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12-APR-2002; 2002EP-00008400
                                                                         22-MAR-2002; 2002JP-00137785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                    ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 370
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 40128; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.8%; Score 559.5; DB 4; Best Local Similarity 39.8%; Pred. No. 2.9e-47; Matches 141; Conservative 56; Mismatches 126;
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                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM04007 standard; protein; 548
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                                                                 Adams M,
                     (PEKE ) PE CORP NY
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                                                                                                                                      N-PSDB; ABL1521
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                                                                 /enter JC,
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Ishii S;
t, Tamechika I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 SIINAKEIMQLLMKGNRQRTQEPTAANQTSSRSHAVLQVTVRQRSRVKNILQEVRQGRLF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDAL-NQGLPR-VPYRDSKLTRLL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide or as a probe for useful in gene therapy. An odeveloping a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM0759-ADM06201 encoded by the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 RVRVAVRLRPF - - VDGTAGAS - - - - - DPPCVRGMDSCSLEIANWRNHQETLK - YQFDAF
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38.9%; Pred. No. 1.9e-47;
ive 70; Mismatches 121; Indels
                                                     Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2692; 305pp; English.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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Matches 132; Conservative
                                                  Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                           WPI; 2003-723558/69.
                                                                                                                                                                                          N-PSDB; ADM01564
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ID ADO.
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cell proliferative disorder; cancer; atherosclerosis; viral infection; HIV; neurological disorder; Parkinson's disease; Alzheimer's disease;
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95. .325
note = kinesin motor domain
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469
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489
/note= "potential phosphorylation site"
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48. .287
note = kinesin motor domain
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97. .399
note= "leucine zipper pattern"
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(INCY-) INCYTE CORP

Ison CH, Nguyen DB; Griffin JA, Burrill JD; ee S, Becha SD, Lee SY; W, Tang YT, Azimzai Y; Swarnakar A, Ho A, Hafalia AJA, Emerling BM, Ison CH, <sup>1</sup> Chien D, Lu DAM, Yang YG, Yue H, Murage J, Griffin JA, Wang JT, Marquis JP, Blake JJ, Chawla NK, Lee S, Becha Richardson TW, Bhatia UG, Zheng W, Sprague WW, Tang YT,

WPI; 2004-305155/28. N-PSDB; ADO44181.

New human structural and cytoskeleton-associated proteins and polynucleotides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cancer, atherosclerosis, HIV or stroke

Claim 1; Page 150-152; 205pp; English.

The present sequence represents a structural and cytoskeleton-associated polypeptide (SCAP). The SCAP polypeptides and polynucleotides of the invention are useful for diagnosing, preventing or treating diseases or conditions associated with aberrant expression of SCAP, such as cell

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                        infections (e.g. HIV) or neurological disorders (e.g. Parkinson's disease, Alzheimer's disease or stroke). These may also be used for assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are also useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide.
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/label= SwitchI motif
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and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
258. .263
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(1). (1) is useful for screening andulators of Hakipad. The method concentration, and assaying for the level of Hakipad activity, where the concentration, and assaying for the level of Hakipad activity, where the Hakipad activity is from binding activity or Arpase activity, where the change in activity between the test and control concentration indicates a modulator. A composition containing (1) is useful in the treatment of inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. hyperplasias, restenosis, cancer, including solid tumours of skin, bream, lung, heart, bone, genitourinary tract, liver, nervous system, adrenal glands, haematologic, gynaecological and testicular carcinomas, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease, proliferation induced after medical procedures, such as surgery, angioplasty. The motor domains may also be used in nanotechnological applications, and polymucleotides encoding the proteins is further useful for inclusion on GeneChip (RTW) array or for use in expression monitoring. This is the amino acid sequence of the novel human contor protein Hakipad motor domain, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel microtubule motor protein for screening modulators of HsKip3d, useful in treatment of hyperproliferative disease e.g. cancer, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease.
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/label= SwitchlI motif /note= "Responsible for sensing of the gamma phosphate and initiating the conformational change between ATP and ADP bound forms of the enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FVDGTAGASDP-----PCVRGMDSCSLEIANWRNHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 3; 66pp; English.
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N-PSDB; ABK10348.
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314 GLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 368

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Search completed: November 5, 2004, 18:44:37 Job time : 78.9417 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	2589	100.0		16	US-10-797-893-4	Sequence 4, Appli
8	2467	95.3	487	16	US-10-797-893-8	Sequence 8, Appli
m	2419	93.4		15	US-10-334-143-80	Sequence 80, Appl
4	2151	83.1		σ	US-09-925-300-1228	•
S	1873	72.3		16	US-10-797-893-2	Sequence 2, Appli
9	1763	68.1		16	US-10-797-893-6	Sequence 6, Appli
7	615.5	23.8		17	US-10-425-115-320209	Sequence 320209,
æ	601	23.2		16	US-10-437-963-159031	Sequence 159031,
0	579	22.4		16	US-10-437-963-103943	Sequence 103943,
10	578.5	22.3		17	US-10-425-115-332919	Sequence 332919,
11	578.5	22.3		15	US-10-425-114-59708	Sequence 59708, A
12	578.5	22.3	1237	15	US-10-334-143-33	Sequence 33, Appl
13	574.5	22.2	_	14	US-10-116-712-670	Sequence 670, App

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       242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
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Publication No. US20040009549A1

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: METHIOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: METHIOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: MIMBER: US/10/334,143

CURRENT APPLICATION NUMBER: US/10/334,143

CURRENT APPLICATION NUMBER: 60/343,169

PRIOR PLING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 207

SOFTWARR: PATENTION VOR: 2.1

SOFTWARR: PATENTION OF SEQ ID NOS: 207

SOFTWARR: PATENTION OF SEQ ID NOS: 207
                                                     327 TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGP
                                                                                                                                                387 VKLSQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLS
                                                                                                                                                                                                                                          447 LDRLLASQGSQGAPLLSTPKRERMVLMKTVEEKDLEIERLKTKQKELEAKMLAQKAEEKE
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                                                                              362 VKLSQKELLGPPEAKRARGPEEEEIGSPEPWAAPASASQKLSPLQKLSSMDPAMLERLLS
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100.0%; Pred. No. 6.6e-195;
cive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 479; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     NHCPTM 512
                                                                                                                                                                                                                                                                                                                                                                                 NHCPTM 487
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US-10-334-143-80
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                                                                                                                                                                      NORSSRSHAVILVKVDQRERLAPFRQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT 300
                                                                                                                                                                                                               241 NORSSRSHAVLLVKVDORERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINT 300
                                                                                                                                                                                                                                                                   SLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSAL 360
                                                                                                                                                                                                                                                                                           301 SLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSAL 360
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                                                                                                                     181 YQEKVLDLLDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRL
2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                                                                                                                                                                             NFAARSKEVINRPFTNESLOPHALGPVKLSQKELLGPPEAKRARGPEEEEIGSPEPMAAP
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95.3%; Score 2467; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.9e-199;
Matches 486; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/10797893
; Sequence 8, Application US/2040142397A1
; GENERAL INFORMATION:
    APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REFERENCE: 1094
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/69/724,224
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; WUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 LEIERLKTKOKELEAKMLAQKAEEKENHCPTM 512
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US-10-797-893-8
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1228
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                    25 GAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQ 84
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                                                                                                                                             APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAION: NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: DO1-08-10
FRIOR PAPLICATION NUMBER: PCT/USOO/05988
PRIOR PAPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VOIL 2.0
SEQ ID NO 1228
LENGTH: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2151; DB 9; Length 4
Pred. No. 2.3e-172;
1; Mismatches 17; Indels
                                                                                                  Sequence 1228, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 LOLGPSACLPGEPXGPSVEYPK 443
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95.9%;
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Best Local Similarity 95.9
Matches 424; Conservative
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63 DPPCVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 FVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGAS
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## Sequence 2, Application US/10797893

| Publication No. US2004014237A1 |
| GENERAL INFORMATION: US2004014237A1 |
| GENERAL INFORMATION: US2004014237A1 |
| GENERAL INFORMATION: US2004014237A1 |
| TITLE OF INVENTION: UNCEL USE |
| TITLE OF INVENTION: Their use |
| TITLE OF INVENTION: UNGER: US/09/724,224 |
| CURRENT APPLICATION NUMBER: US/09/724,224 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-06-20 |
| PRIOR FILING DATE: 2000-06-20 |
| PRIOR FILING DATE: 2000-06-20 |
| PRIOR FILING DATE: 2000-06-20 |
| SEQ ID NOS: 8 |
| SOFTWARE: PSECENT OF Windows Version 4.0 |
| SEQ ID NO S: Windows Version 4.0 |
| THENGTH: 370 |
| THENGTH: 370 |
| THENGTH: MANNAR HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HUMAN HU
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Fublication No. US20040142397A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
FILE REPERENCE: 1004
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/09/724,224
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-12-8
PRIOR FILING DATE: 2000-06-20
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100.0%; Pred. No. 4.6e-149;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 369; Conservative
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Sequence 159031, Application US/10437963
; Bedience 159031, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Abou, Yihua
    APPLICANT: Abou, Yougwei
    APPLICANT: Boucharov, Andrey A.
    APPLICANT: Boucharov, Andrey A.
    APPLICANT: Barbazuk, Brad
    APPLICANT: Barbazuk, Brad
    APPLICANT: Barbazuk, Brad
    APPLICANT: Barbazuk, Brad
    APPLICANT: Li, Ping
    APPLICANT: 
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      273 ISALNKNEHRIPYRQSKLTRLLRDSLGGGSRTVMIACLNPAE--YQESANTVSLAARSCH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 IEN--FTSSSKQETPKLKIDMEAKLRAWLESKGKTKSIQRMDGLFSPIASKTPLSVSHMK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 QPTSSRIPCRVKAMDQDGGKIKKILFDDVVHVPTENIPREHRQTEVNTPKKVVLPSVTPC 448
                                                                                                                                                                                                                            AVILVKVDORERLAPPROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKV 308
                                                                                                                                                                                                                                                                                                                                                    309 VDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPLL---STPKRERMVL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 NEKHEASLRKALSPIS--SNMVP-----VEQQIPDNGN--CPVLLEPQTPIEKRNIV 496
                                                                                                                                                                                                                                                                LDPASGDLVIREDCRGNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSH
                                                                                                                                                              159 LEPKAKEIMALDÜKDĞNMQLKĞLSWVPVRSMEEPQELYSIGVQRRKVAHTGLNDVSSRSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 VINRPFTNESLQP-------HALGPVKLSQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_58448C.1.pep
US-10-437-963-159031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 MKTVEEKDLE-IERLKTKQKE-----LEAKMLAQKAE 503
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OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Oryza sativa
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LOCATION: (1)..(3
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US-10-437-963-159031
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326,
SEQ ID NO 320209
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
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                                                                                                                                                                                                                                                         68.1%; Score 1763; DB 16; Length 346; 100.0%; Pred. No. 7.8e-140; ive 0; Mismatches 0; Indels 0
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US-10-425-115-320209
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
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                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human
US-10-797-893-6
                                                                                                 LENGTH: 346
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Matches 181;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yougwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 322919
LENGTH: 783
                                              : | | | | | | | | | :::||||:
453 RTQRSIEGANINRSLIALSSCINALVEGKKHIPYRNSKLTQLLKDSLGGSCNTVMIANIS 512
                                                                                                                                                                               403 ARGPEEERIGSPEPMAAPASASOKLSPLOKLSSMDPAMLERLLSLDRLLASOGSOGAPLL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 NETVRDLLSPGS-PLNLREDKQG-IVAAGLTQRSVYSTDEVMELLQKGNKNRTTEPTRVN 405
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                            KGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIA
                                                                                                                          348 PERRFYLDTVSALNFAARSKEVINRPFTNESLQPHALGPVKLSQKELL-----GPPEAKR
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                                                                                                                                                                                                          573 QLARQQQKLLIVQAQTLASNASPQQSPAPSAQISTPCSTQRKVKRSILAGN---
                                                                                                                                                                                                                                                                                     STPKRERMV-----LMKTVEEKDLEIERLKTKQKELEAKMLAQKAE 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.3%; Score 578.5; DB 17; Length Best Local Similarity 32.9%; Pred. No. 1.8e-39; Matches 167; Conservative 94; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: MRT4577_66737C.1.pep
US-10-425-115-332919
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OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 332919, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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LOCATION: (1)..(
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221) B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 103943
                                                                                                                                                     QLKGLAWVVVRSLEEFHEIYSIGVQRRKVAHTGLNDVSSRSHAVLSIRITT-----DV 220
                                                                                                                                                                                                                                                                                                  12,
                                                           118 IMXSTVLALCTGT-----WC-SVEISYYEVYMERCYDLLEPKAREIMVLDDKDGNL 167
                                                                                                                                                                                                                  ECYKLDAFFGQESRVCEIFDQEVSAVIPGIFEGTNATVFAYGATGSGKTYTMQGTEDLPG 117
                                      147 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 206
                                                                                                                  207 LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 266
                                                                                                                                                                                                267 REGKLYLI---DLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRD 323
                                                                                                                                                                                                                                                                           SKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVINRPFTNESLQPHA 383
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                                                                                                                                                                                                                                                                                                                                                       384 LGPVKLSOKELLGPPEAK-----RARGPEE-----EEIGSPEPMAAPASASQ 425
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22.4%; Score 579; DB 16; Length 77
Best Local Similarity 30.6%; Pred. No. 1.6e-39;
Matches 162; Conservative 100; Mismatches 209; Indels
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US-10-437-963-103943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 103943, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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US-10-116-712-670
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APPLICANT: Zhou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
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FAARSKEV---INRPFTNESL--OPHALGPVKLS-OKE--LLGPPEAKRARGPEEEIGS 413
                                     414 PEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLLASQGSQGAPILLS----TPKRER 469
                                                                                                                                                               581 AEAQLLASKTSPQRSPAPPSHVSTPGSTQRKTRRSILAAGGGNYFSKLDSKRHAADNAQV 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-256-H1_FLI.pep
US-10-425-114-59708
                                                                                                                                                                                                                                       470 MVLMKTVEEKDLEIERLKTKQKELEAK 496
                                                                                                                                                                                                                                                                                            641 RELORKVSTLESEIEKMK-KEHLLOLK 666
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59708, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Matches 167; Conservative
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR--VPYRD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 LGPVKLISQKELLGPPEAKRARGPEEEIGSPEPMAAPASASQKLISPLOKLSSMDPAMLER 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                          US-10-34-143-33

Sequence 33, Application US/10334143

Sequence 33, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:
APPLICANT: GRICORIEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REWOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED MITH THE METHOD
FILE REFERENCE: 036602/1543
CURRENT APPLICATION NUMBER: US/10/334,143

CURRENT FILING DATE: 2002-12-31

PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 VRVAVRLRPFVDGTAGASDPPC-----VRGMDSCSLEIANWRNHQETLKYQFDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VRVALRCRPLVPKEISEGCQMCLSFVPGETQVVVGTDK------SFTYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 IPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYOEKVLDLLDPA--SGDLVIREDCRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AELNHLKQ-----QVQQLQVLLLQAHGGTLPGSINAEPSEN---LQSLMEKNQSLVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 LLSLDRLLASQGSQGAPLLSTPKRERMVLMKTVEEK-DLEIERLKTKOK-ELEAKMLAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.3%; Score 578.5; DB 15; Length Best Local Similarity 32.4%; Pred. No. 3.5e-39; Matches 157; Conservative 97; Mismatches 172; Indels
                          470 MVLMKTVEEKDLEIERLKTKQKELEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 670, Application US/10116712; Publication No. US20030194764A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-334-143-33
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

5, 2004, 18:34:12 / Search time 10.0875 Seconds November Run on:

(without alignments)
3300.235 Million cell updates/sec

1768 1 MGRCRLSKIGATRRPPPARV....FYLDTVSALNPAARSKEVIN 346 US-10-797-893-6 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_79:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIES

	Description	kinesin-like DNA b	kinesin-like prote	kinesin-related pr	F25116.11 protein	kinesin heavy chai	probable kinesin-1	kinesin-like prote	F22M8.8 protein -	KLP2 protein - Afr	kinesin homolog F2	probable kinesin-r	kinesin-related pr	kinesin-related pr	-	kinesin-related pr	kinesin-related pr		kinesin-related pr		chromokinesin - ch	kinesin-related pr		kinesin homolog KH	kinesin-related pr	kinesin-like prote	microtubule-associ	kinesin heavy chai	kinesin-like prote	
SUMMARIES	ID	\$62328	T48258	A55236	A86319	T18277	T40594	151617	D86151	T30335	T06733	H84777	T47525	T02017	B84687	538982	A48669	A56921	B44259	S64238	A56514	A57107	E84792	A53939	T14156	T48959	A54803	T10164	B48835	T46242
	DB	7	~	-	~	~	7	~	7	~	7	~	~	~	~	ч	н	~	н	~	7	-	~	~	~	~	~	~	7	~
	Length	665	664	784	703	1254	784	1226	882	1388	1070	1056	1058	1006	1076	669	1066	1695	701	802	1225	747	1022	786	2954	1229	1231	928	330	813
46	Ouery Match	87.7	33.6	31.4	31.1	30.9	30.3	30.1	30.0	29.8	29.7	29.6	29.6	29.5	29.5	29.1	29.1	29.1	29.0	29.0	29.0	29.0	28.9	28.8	28.8	28.7	28.7	28.7	28.5	28.5
	Score	1550	594.5	555.5	550	547	536	532	530.5	527.5	525	524	523	521.5	515.5	514.5	514	514	513.5	513.5	513.5	513	511.5	509.5	509.5	208	507.5	507	504.5	504
	Result No.	-	7	e	4	S	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

kinesin-like spind	kinesin-like prote	kinesin [imported]	hypothetical prote	nesin [imported]	kinesin heavy chai	kinesin-related pr	kinesin-like heavy	kinesin-related pr	kinesin heavy chai	kinesin-like prote	kinesin-like prote	kinesin-related pr	kinesin-like prote	kinesin heavy chai	cinesin heavy chai	
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G02157	A55289	T51930	T20621	T51932	A41919	558691	T51360	JC5831	S44868	C48835	T40128	JN0114	T15822	837711	A38713	
H	ч	~	~	7	н	н	~	7	~	~	~	-	~	~	-	
1056	1150	932	958	929	963	742	987	793	843	332	883	1584	1584	1027	1031	
28.3	28.3	28.2	28.0	28.0	27.8	27.7	27.6	27.5	27.5	27.3	27.3	27.3	27.3	27.3	27.3	
501	200	498.5	495.5	495	491	490	. 488	485.5	485.5	483	482.5	482.5	482.5	482	482	
30	31	32	33	34	35	36	37	38	39	, 40	41	42	43	44	45	

## ALIGNMENTS

Accession: 1ike DNA binding protein KID - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Ja-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Aug-2004
C;Accession: 56228
R;Tokai, N.; Fujimoto-Nishiyama, A.; Toyoshima, Y.; Yonemura, S.; Tsukita, S.; Inoue, J. BrNG J. 15, 457-467, 1996
A;Title: Kid, a novel kinesin-like DNA binding protein, is localized to chromosomes and A;Reference number: 56228; MUID:96174806; PMID:859929
A;Reference number: 56228
A;Accession: 56228
A;Accession: 56228
A;Accession: 56228
A;Accession: 56228
C;Superfaminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-665 <TOK>
C;Superfamily: kinesin motor domain homology
C;Keywords: ATP; nucleotide binding; P-loop
F;44-374/Domain: kinesin motor domain homology
F;128-135/Region: nucleotide-binding motif A (P-loop)

Gaps 2 Length 665; Query Match 87.7%; Score 1550; DB 2; Length 6. Best Local Similarity 90.8%; Pred. No. 1.6e-117; Matches 314; Conservative 1; Mismatches 29; Indels

7

85 61 26 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 셤 ò

62 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAS-VLAYGPTGAGKTHTMLGSPEQP 120 86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNAKVVLAYGPTGAGKT-THAGQPRAT 144 셤 ò

180 145 WGDPAGSHGPPAAHKGGCRGPAMGLSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGN 204 121 GVIPRALMDLLQLTREEGAEGRPWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGN ઠે ద

181 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 240 205 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR 264 ઠે g 241 QREGKLYLIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300 265 ð 요 δ

301 LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346

,325

T48258 Kinesin-like protein - Arabidopsis thaliana N,Alternate names: protein T1E22.130



```
Kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)

NyAlternate names: kinesin-like protein 5; KLP5
C; Species: Drosophila melanogaster
C; Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C; Accession: A55236; E41298
R; Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Cell Biol. 127, 1041-1048, 1994
A; Title: Characterization of the KuP68D kinesin-like protein in Drosophila: possible rol
A; Reference number: A55236; MUD: 95050960; PMID: 7525600
A; Residues: 1-784 <-PES>
A; Rocession: A55236
A; Molecule type: mRNA
A; Residues: 1-784 <-PES>
A; Cross-references: UNIPROT: P46867; GB: U15974; NID: 9595912; PIDN: AAA69929.1; PID: 9555096
B; Residues: 1-784 <-PES>
A; Cross-references: UNIPROT: P46867; GB: U15974; NID: 9595912; PIDN: AAA69929.1; PID: 9555096
B; Residues: 1-784 <-PES>
A; Cross-references: US: A: 88, 8470-8474, 1991
A; Reference number: A41298; MUD: 92020874; PMID: 1924306
A; Molecule type: DNA
A; Residues: 'TC', 222-337, 'VRGQV' <-STE>
A; Cross-references: GB: M74431; NID: 9157791; PIDN: AAA28658.1; PID: 9157792
A; Cross-references: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBase: FlyBas
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24489
A;Reference number: Z24489
A;Residue: T4828
A;Residue: Pred call and A
A;Residues: L64 cBLV.
A;Residues: L64 cBLV.
A;Residues: L64 cBLV.
A;Residues: L64 cBLV.
A;Residues: L64 cBLV.
A;Cross-references: UNIPROT:O9LZ88; EMBL:AL162874
A;Experimental source: cultivar Columbia; BAC clone T1E22
C;Genetics:
A;Map position: 5
A;Introns: 58/3; 128/2; 184/3; 310/1; 378/3; 480/2; 501/3; 535/1; 607/3; 628/3
A;Note: T1E22.130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 SVPVKŚMSEPQEAYLCGVQRRKVAHTGLNDVSSRSHGVLVISVTSQGLVT-----GKIN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQD 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 ARVRVAVRLRPFV----DGTAGASDPPCVRGMDSCSLEIANWRNHQETLK---YQFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%; Score 594.5; DB 2; Length 38.6%; Pred. No. 4.2e-40; Live 69; Mismatches 114; Indels
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Matches 131; Conservative
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PS5116.11 protein - Arabidopsis thaliana (G.) Species: Arabidopsis thaliana (mouse-ear cress) (C.) Species: Arabidopsis thaliana (mouse-ear cress) (C.) Species: Arabidopsis thaliana (mouse-ear cress) (C.) Species: O. Mar. 2001 #sequence_revision.02-Mar. 2001 #text_change 09-Jul-2004 (C.) Accession: A86319 (C.) R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso., Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huzar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, C.A.; Liu, S.X.; Liu, Z.A.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rowley, T.; Rowley, D.; Sakano, H. A.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Liu, S.X.; M.; Mu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis. A.; Reference number A86319 A.; Status; preliminary
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C;Genetics:
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9
A;Description: may be part of a motor protein that provides anterograde fast ax C;Superfamily: kinesin-related protein KF3; kinesin motor domain homology C;Keywords: AFP; coiled coil; microtubule binding; nucleotide binding; P-loop F;1-349/Domain: head globular #status predicted <HG1:-F;20-350/Domain: kinesin motor domain homology <KMOT>F;106-113/Region: nucleotide-binding motif A (P-loop) F;350-580/Domain: helical rod #status predicted <HGD>F;350-580/Domain: tail globular #status predicted <HGD>F;112/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP 292
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                                                                                                                                                                                                                                                                                                                                                                                         31,
                                                                                                                                                                                                                                                                                                                          Length 784;
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                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                          31.4%; Score 555.5; DB 1;
39.5%; Pred. No. 7.7e-37;
tive 56; Mismatches 127;
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Matches 140; Conservative
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Kinesin-like protein 1 - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004 R;Vernos, I.; Raats, J.; Hirano, T.; Heasman, J.; Karsenti, B.; Wylie, C. Cell 81, 117-127, 1995 Hirano, T.; Heasman, J.; Karsenti, B.; Wylie, C. Arities: XIDI, a chromosomal Xenopus Kinesin-like protein essential for spindle organi A;Reference number: A56221; MUID:95236444; PMID:7720067
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT: Q91784; EMBL:X82012; NID:g562792; PIDN:CAA57539.1; PID:g562
B;Vernos, I.; Heasman, J.; Wylle, C.
B;Vernos, I.; Heasman, J.; Wylle, C.
B;Vernos, I.; Heasman, J.; Wylle, C.
B;Vernos, I.; Heasman, J.; Wylle, C.
A;Vernos, I.; Heasman, J.; Wylle, C.
A;Title: Multiple kinesin-like transcripts in Xenopus occytes.
A;Reference number: A48835; MUID:93246065; PMID:8482413
A;Accession: A48835
A;Status: preliminary; not compared with conceptual translation
                                                                                                                  GSPDB:GN00067; SPDF
                                   A, Molecule type: DNA
A, Residues: 1-784 <- PUR>
A, Residues: 1-784 <- PUR>
A, Residues: 1-784 <- PUR>
A, Residues: 1-784 <- PUR>
A, Experimental source: strain 972h-; cosmid c649
B, Robert and source: strain 972h-; cosmid c649
R, Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
R, Monitted to the EMBL Data Library, July 1998
A, Reference number: Z21861
A, Reference number: Z21861
A, Rolecule type: DNA
A, Molecule type: DNA
A, Residues: 464-784 <- WOO>
A, Cross-references: EMBL: AL031154; PIDN: CAA20063.1; GSPDB: GN00067; SPDB: SPBC1685.15c
C, Generics: strain 972h-; cosmid c1685
C, Generics: SPDB: SPBC649.01c; SPDB: SPBC1685.15c
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Matches 139; Conservative
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       T40594
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A, Introns: 11/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinesin heavy chain - slime mold (Dictyostellum discoideum)

C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
R;deHostos, E.L.; McCaffrey, G.; Vale, R.D.
R;deHostos, E.L.; McCaffrey, G.; Vale, R.D.
A;Recreace number: Z18853
A;Recession: T18277
A;Retreace number: Z18853
A;Recession: T18277
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1254 v.DEH>
A;Cross-references: UNIPROT:Q94463; EMBL:U41289; NID:g1526990; PID:g1526991; PIDN:AAB077
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40594; T39531
R;Purnelle, B.; Goffeau, A.; Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, May 1998
A;Reference number: Z21939
                                                                                                           189
321
                                                                                                                                                                                                                                       PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR--QREGKLY 247
                                                                                                                                                                                                                                                                                                                      367
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                                                                                                                                                                                                                                                                                                                                                                                                                      74 STOQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMDL--- 130
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                                                                                                                                           LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%; Score 547; DB 2; Length 1254; larity 36.3%; Pred. No. 7.2e-36; Conservative 76; Mismatches 126; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
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GNSKTSLIINCSPSNNNEHETITTLQFGTRAKTINN 351
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Best Local Similarity
Matches 122; Conserv
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A;Residues: 1-1388 <BOL>
A;Cross-references: UNIPROT:Q91785; EMBL:X94082; NID:g1129172; PID:e213754; PIDN:CAA638;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KID? protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 16-Aug-2004
C;Date: 22-Oct-1999 #sequence_revision in the controsome R;Boleti, H.; Karsenti, E.; Vernos, I.
R;Boleti, H.; Karsenti, E.; Vernos, I.
Cell 84, 49-59, 1996
A;Title: A new Xenopus centrosomal kinesin-like protein required for centrosome A;Reference number: Z20827; MUID:96140639; PMID:8548825
A;Accession: T30335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQP-----GVIPRA--- 126
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                                                                                                                                                                                                                                                                                                                                 273 SUVENEFPUSNEMESSSHFURPSKPLVRRSKLVLVDDAGSERVHKSGSEGHMLEEAKSIN 332
                                                                                                                                                                                                                                                                                                                                                                                                          TSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ESVPSSVAKNIVESCANGYNGTIFAYGQTGSGKTFTMLGPSESDNFTHNLRGVIPRSFEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 SQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKVDQRERLAPF-RQREGK
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                                                                                                                                                                                            174 REDCR-GNILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNORSSRSHAVLLVKV--
                                                                                                                                                                                                                         20 VRVAVRLRPFVDGTAGASDPP---CVRGMDSCSLEIANWRNHQETLKYQFDAFYGERSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 SPEQP--GVIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI
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29.8%; Score 527.5; DB 2;
Best Local Similarity 36.5%; Pred. No. 3.2e-34;
Matches 126; Conservative 68; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSSSASIGAADNGVPGRVRVAVRLRPRNADESVADADFADČVELQPELKRLKLRKNNNM-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOODIYAGSVQPILRHILEGQNASVLAYGPIGAGKTHTMLGS-----PEQP--GVIPRAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDLLQLTREEGAEGRP-WALSVIMSYLEIYQEKVLDLLDPA---SGDLVIREDCRGNILI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPR---VPYRDSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCRLSKIGATRRPPPARVRVAVRLRP--FVDGTAGASDPPCVR---GMDSCSLEIANWRN 57
                                                                                                                                                                                                                                                                                                                                                                                                    74
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQETL----KYQFDAFYGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRVALRCRPLVP------KENNEGCKMCLIFVPGEQQVIVGTEKSFTYDYVFDPSA
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                                                                                                                                                                                                                                                                                                                                               34;
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30.0%; Score 530.5; DB 2; Length 885;
Best Local Similarity 36.3%; Pred. No. 9.6e-35;
Matches 135; Conservative 66; Mismatches 132; Indels 39
                                                                                                                                                                                                                                                                                       Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTRILODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%; Score 532; DB 2; Length 12
36.1%; Pred. No. 1.1e-34;
ive 74; Mismatches 113; Indels
                A, Residues: 9-162,'L', 164-338 <VE2>
A, Experimental source: oocyte
A, Note: sequence extracted from NCBI backbone (NCBIP:130975)
C, Genetics:
A, Gene: klp1
C, Superfamily: kinesin motor domain homology
C, Keywords: ATP; nucleotide binding; P-loop
C, Keywords: ATP; nucleotide binding; P-loop
F, 9-343/Domain: kinesin motor domain homology <KMOT>
F, 87-94/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.1%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
Molecule type: DNA
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C;Genetics:
A;Map position: 1
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143

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A;Introns: 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1;
A;Note: F16L2.60
C;Superfamily: Kinesin-related protein KIP1; Kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unseld, M.; Mewes, H.W.; Rudd,
                                                                                                                                                                  141 TYTWEGGARKKNGEFPSDAGVIPRAVKQIFDILEAQGAE----YSWKVTFLELYNEEIS 195
                                                                                                                                                                                                                                                                                                                                173 IREDCRGNILIPGLSQKPISS----PADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         INQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLLDP-----ASGDLVIREDCRGNILIPGLSQXPISSFADFERHFLPASRNRTVG 211
                                                                       31 RSSESNSTWRNDKEKGVNVQVILRCRPLSEDEARIHTPVVI----SCN-----ENRREV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinesin-related protein-like - Arabidopsis thaliana
NiAlternate names: protein F1612.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47525
R;Jordan, N. Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W submitted to the Protein Sequence Database, March 2000
A;Reference number: 224468
                                                                                                                                                                                                                                                                                                                                                             VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRN----HOETLKYOFDAFYGERST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKYQ------FDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLSKIGATRRPPPAR----VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
  Gaps
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  44;
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Indels
                                                                                                                                          QQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS---
                                                                                                                                                                                                                                     PRALMDLLQLTREEGAEGRPWALSVTMSYLETYQEKVLDLLDP-
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A,Cross-references: UNIPROT:Q9LZU5; EMBL:AL162459
A,Experimental source: cultivar Columbia; BAC clone F16L2
Mismatches 118;
67;
131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: T47525
A, Status: preliminary
A, Molecule type: DNA
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A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: H84777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1056 <STO>
A;Cross-references: UNIPROT:P82266; GB:AE002093; NID:94510356; PIDN:AAD21445.1; GSPDB:GN
                                                                                   C, Accession: T06733
R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu submitted to the Protein Sequence Database, April 1999
A;Reference number: 215793
A;Accession: T06733
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Arabidopsis thalians (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H8477;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
                                                                                                                                                                                                                           A;Residues: 11070 cQUE>
A;Residues: 11070 cQUE>
A;Cross-references: UNIPROT:09SV36; EMBL:AL049655; GSPDB:GN0061; ATSP:F28P10.150
A;Cross-references: UNIPROT:09SV36; EMBL:AL049655; GSPDB:GN0061; ATSP:F28P10.150
G;Genetics:
A;Gene: ATSP:F28P10.150
A;Map position: 3
A;Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3; C;Superfamily: kinesin-related protein KLP61F; kinesin motor domain homology
F;124-466/Domain: kinesin motor domain homology cRMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKV----DQRERLA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-----RQREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inesin homolog F28P10.150 - Arabidopsis thaliana
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARVRVAVRLRPFVDGTAGASD------PPCVRGMDSCSLEIANWRNHQETLKYQFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.7%; Score 525; DB 2; Length 10 Best Local Similarity 35.3%; Pred. No. 3.5e-34; Matches 126; Conservative 69; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 524; DB 2;
Pred. No. 4.1e-34;
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36.4%;
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Best Local Similarity
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109 128

DPASGDLVIREDCRG

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A; Cross-references: UNIPROT: Q9SIB3; GB: AE002093; NID: g4580395; PIDN: AAD24373.1; GSPDB:GRC; Genetics:
                                                                                                                                                                                                                                                                                                                                                                    170 QIFDILEAQSAA----EYSLKVSFLELYNEELTDLLAPEETKFADDKSKKPLALMEDGKG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RO--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEIVKSGKLNLVDLAGSENISRSGAREGRAREAGEINKSLLTLGRVINALVEHSGHIPYR 345
                                                                                                                                                                                                                                                                                QDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS-----PEQPGVIPRALM
                                                                                                                                                                                                                                                 20 VRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIA---NWRNHQETLKYQFDAFYGERSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 2
C;Superfamily: kinesin-related protein KIP1; kinesin motor
                                                                                                                                                      29.2%; Score 515.5; DB 2; 35.0%; Pred. No. 2.1e-33; iive 68; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLL-
                                                                                                                                                                              Best Local Similarity 35.09
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-699 <COL1>
<STO>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S38982
1-1076
                                                                A; Gene: At2g28620
                                                                                                                                                                                                                                                                                                 21
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                                                                                                                                                                                                                                                                                                               R; Asada, T.; Kuriyama, R.; Shibaoka, H.
J. Cell Sci. 110, 179-189, 1997
A; Title: TKRP125, a kinesin-related protein involved in the centrosome-independent organ
A; Reference number: Z14490; MUID:97196959; PMID:9044048
A; Accession: T02017
A; Sccession: T02017
A; Wolccule type: mRNA
A; Wesidues: 1-1006 <ASA>
A; Residues: 1-1006 <ASA>
A; Conetics: Conetics: UNIPROT:023826; EMBL:D83711; NID:g2582970; PIDN:BAA23159.1; PID:g258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable kinesin-like spindle protein [imported] - Arabidopsis thaliana (fispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispace: O2-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Ciscossion: B84687
Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; FMID:10617197
A;Accession: B84687
A;Accession: B84687
A;Accession: B84687
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 LNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
SGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLGGSAHSILIANIAPERRFYL 329
                     :| || || || :| :| | : || : || || AGEINKSLLTLGRVINALVEHSGHIPYRDSKLTRLLRESLGGKTKTCVIATISPSIHCLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOODIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGS------PEQPGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- ASGDLV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 IREDCRGNILIPGLSQKPISS----FADFERHFLPASRNRTVGATRLNQRSSRSHAVLLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 KVDQRERLAPFRQ--REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VQVLLRCRPPSNDELRNNAPQVVTCNDYQREVAVSQNIAG--KHIDRI-FTFDKVFGPSA 66
                                                                                                                                                                                                                                                 inesin-related protein TKRP125 - common tobacco
Species: Nicotiana tabacum (common tobacco)
Jate: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VRVAVRLRPFVDGTAGASDPPCVRGMD----SCSLEIANWRNHQETLKYQFDAFYGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : || :| :| :| || :: :: |
182 IMEDGKGGVIVRGLEEEIVTSANEIFTLLER----GSAKRTAETILINKQSSRSHSLFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: kinesin-related protein Eg5, kinesin motor domain homology;10-361/Domain: kinesin motor domain homology <RMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 IPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.5%; Score 521.5; DB 2; Best Local Similarity 35.6%; Pred. No. 6.2e-34; Matches 128; Conservative 69; Mismatches 118;
                                                                                                              :|:| |::| |:|
376 ETLSTLDYAHRAKNIKN 392
                                                                                      DTVSALNFAARSKEVIN 346
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                                        316
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(PIR:S5869)
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A,Accession: S72551
                                                                                                                                                                                                                            egga
                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Residues: 2-5, X*, 7-11; 99-64; 125-132; 222-226, X*, 228-230 <COL2> A; Residues: 2-5, X*, 7-11; 90-64; 125-132; 222-226, X*, 228-230 <COL2> C; Complex: heterotrime of a 115K chain and two kinesin recorded KIP3; kinesin motor domain homology C; Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-10op F; 97-104/Region: nucleotide-binding motif A (P-10op) F; 97-104/Region: nucleotide-binding motif A (P-10op)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQDIYAGSVQPILRHİLEGQNASVLAYGPTGAGKTHTMLG---SPEQPGVIPRALMDLLQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinesin-related protein KRP85 - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: kinesin-2 chain A; KRP (85/95) 85K chain
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-58p-1999 #sequence_revision 10-5ep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VRVAVRLRPFVDGTAGASDPPCVRGMDSC--SLEIANWR--NHQETLKYQFDAFYGERST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VRVVVRCRPLNSKETGQGFKSVVK-MDEMRGTVQVTNPNAPSGEPPKSFTFDTVFAPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 514.5; DB
Pred, No. 1.4e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.1%;
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Search completed: November 5, 2004, 18:45:33 Job time : 11.0875 secs This page Blank (uspto)

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5, 2004, 18:34:12; Search time 71.0157 Seconds (without alignments): 1747.786 Million cell updates/sec
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1 MGRCRLSKIGATRRPPPARV......FYLDTVSALNFAARSKEVIN 346
5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                        2002273 seqs, 358729299 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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geneseqp2001s: geneseqp2002s: geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* A\_Geneseq\_23Sep04:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	kin	mic	kin	mic	kin	mic.	hum	kin	mic	KNS	pro	ohil	pro	tura	hum	cell	hum	nov	ЬÞ	MDD	hum	phi1	da a	da a	da a
и	Human	Human	Human	Human	Human	Human	Novel	Human	Human	Human	Human	Drosophil	Human pro	Structura	Novel hum	Intracell	Novel	Human	Human	Human MDD	Novel	Drosophil	Candida	Candida	Candida
Description	Adc23342	Adq60232	Adc23344	Adq60234	Adc23338	Adq60228	Adk40973	Adc23340	Adq60230	Adq09240	Aab56650	Abb71112	Adm04007	Ado44167	Aau76958	Abu53123	Aau 76957	Adc31082	Adi15915	Abu11606	Aau76967	Abb65183	Adn40550	Adn40554	Adn40548
	), ),																								
QI	ADC23342	ADQ60232	ADC23344	ADQ60234	ADC23338	ADQ60228	ADK40973	ADC23340	ADQ60230	ADQ09240	AAB56650	ABB71112	ADM04007	AD044167	AAU76958	ABU53123	AAU76957	ADC31082	ADI15915	ABU11606	AAU76967	ABB65183	ADN40550	ADN40554	ADN40548
80	7	œ	2	8	7	œ	7	7	8	80	٣	4	7	œ	Ŋ	4	Ŋ	7	7	9	S	4	8	8	8
Length DB	346	346	487	487	370	370	490	512	512	665	460	784	548	966	357	868	868	898	868	603	905	677	408	408	972
Query Match	100.0	100.0	100.0	100.0	99.7	99.7	99.7	99.7	99.7	99.7	99.2	31.6	31.6	31.6	31.2	31.2	31.2	31.2	31.2	31.2	31.1	30.3	30.1	30.1	30.1
Score	1768	1768	1768	1768	1763	1763	1763	1763	1763	1763	1753	559.5	559	559	552.5	552.5	552.5	552.5	552.5	551.5	549	535.5	532.5	532.5	532.5
Result No.		7	٣	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP to phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a

Adn40552 Candida a	Abb07412 Amino aci	Abg72053 Human H8K	Human	Abg72052 Human kin	Human	Human	Aae14401 Human HsK	Human	Нишап	Adc31540 Human nov	Humar	Aau79590 Human kin	Humar	_	Adc35116 Human bre	Adl83290 Human PRO	Adq20128 Human sof	Нишап	Adj95078 Novel NOV
ADN40552	ABB07412	ABG72053	ABB07410	ABG72052	AAU19569	ABP51294	AAE14401	AAE14402	AAU79592	ADC31540	AAE14400	AAU79590	ABR48222	ADB80468	ADC35116	ADL83290	ADQ20128	ADQ09226	ADJ95078
œ	ß	9	ഹ	9	4	S	Ŋ	Ŋ	2	7	ß	Ŋ	ø	7	7	æ	æ	ω	7
974	383	383	864	864	757	757	375	409	409	419	1388	1388	1388	1388	1388	1388	1388	1388	834
30.1	29.9	29.9	29.9	29.9	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.6
532.5	528	528	528	528	527	527	526	526	526	526	526	526	526	526	526	526	526	526	523.5
26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostetic; cardiant; immunomodilator; antlinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation. This invention relates to a novel method for high throughput screening Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate. Human kinesin-like DNA binding protein (KID) (SeqID 6). Claim 1, SEQ ID NO 6, 26pp; English. ADC23342 standard; protein; 346 AA. 28-NOV-2000; 2000US-00724224. 20-APR-1999; 99US-00295612. 20-JUN-2000; 2000US-00597292. (first entry) (CYTO-) CYTOKINETICS INC. WPI; 2003-706919/67. N-PSDB; ADC23341. US6387644-B1. Homo sapiens. 18-DEC-2003 14-MAY-2002. Beraud C; ADC23342; ADC23342 

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kinesin-like DNÀ binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatement of cancer, hyperplasias, restenosis, cardiac hypertraphy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 6) of the invention.
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                                                                                                                               Score 1768; DB 7;
Pred. No. 1.2e-173;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 346; Conservative
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                                                                                                    Sequence 346 AA;
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening corformidated Arpase activity, a method of testing for Arpase activity of microtubule estimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention.
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restenosis, cardiac hypertrophy, immune disorders and
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    hyperplasias,
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Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
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                                              Human microtubule motor protein #4.
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28-NOV-2000; 2000US-00724224.
                  (first entry)
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                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polypeptide sequence is human KID protein (SeqID 8) of the invention.
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protein for treating cellular proliferation disorders by adding a
candidate agent to a mixture of the target protein that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1768; DB 7; Length 487; 100.0%; Pred. No. 2.1e-173; Live 0; Mismatches 0; Indels 0
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20-JUN-2000; 2000US-00597292
                                                       28-NOV-2000; 2000US-00724224
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Best Local Similarity 100.
Matches 346; Conservative
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99US-00295612.

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for Muduators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for correcting for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune disorders and inflammation, for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and profession associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and consideration induced after medical procedures and co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQE
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Matches 346; Conservative
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ADQ60234 standard; protein; 487 AA.

ADQ60234

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia, restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                       86 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                               62 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                                                          LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                      GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                  GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                                                                                   122 VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
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                                                          Indels
           Score 1763; DB 7; I
Pred. No. 4.5e-173;
                                                          Mismatches
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99.7%; sc.
100.0%; Pred
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-SEP-2004 (first entry)
                Query Match
Best Local Similarity 100.
Matches 345; Conservative
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                                                                                                                                  241 QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human, enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for high throughput screening
                                            181 ILIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFR
                                                                                                         QREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                                                                           LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                  LTRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinesin-like DNA binding protein (KID) (SeqID 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by ATGCA"
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20-JUN-2000; 2000US-00597292.
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31-DEC-2002; 2002WO-US041687 31-DEC-2001; 2001US-0343169P

WO2003057841-A2 17-JUL-2003 ŝ

Grigoriev IV, Sudarsanam

GRIGORIEV I V. (SUDA/) SUDARSANAM S.

(GRIG/)

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contivity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target.

Control or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA chinding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune associated with KID and for inhibiting KID and for treating autoimmune confiseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
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Sequence 370 AA;

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LKYQPDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121
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                                                                                                                GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHOET
                                                              VI PRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                  146 VIPRALMDLLQLTREEGAEGREWALSVTWSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                                                                                                                                                                                                 LI PGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                               REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL
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99.7%; Score 1763; DB 8; Length 370; 100.0%; Pred. No. 4.5e-173; tive 0; Mismatches 0; Indels C
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Matches 345;
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antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; fimunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia;
                                                                                                                                                                       cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                     metabolic disorder; organ transplant rejection; enzyme
ADK40973 standard; protein; 490 AA
                                                                                                                             Novel human kinase protein #80.
                                                                                  06-MAY-2004 (first entry)
                                          ADK40973;
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The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and conditions to (a) and conditions to (b) the conditions to (b) and conditions to (c) is a complement of (d). The nucleic acid molecules, configurably cancers in munune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are conversably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, pain, conversing tiffections caused by prions, infections caused by prions, infections caused by fungi, ocular diseases, migraines, pain, causorders, hypotension, mood disorders, attention disorders, pain, causorders, hypotension, hypertension, psychotic disorders, neurological cisorders, dyskinesias, metabolic disorders and organ transplant rejection. This sequence corresponds to one of the kinase polypeptides of the invention.
                                                                                                                                                                                                                                                                                                      New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 80; 491pp; English.
                                                                                                                                                                                                                                                                                                                                                                      metabolic disorders.
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Query Match 99.7%; Score 1763; DB 7; Length 490; Best Local Similarity 100.0%; Pred. No. 6.9e-173; Matches 345; Conservative 0; Mismatches 0; Indels 0

Gaps

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LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 121 153 181 241 274 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNGGLPRVPYRDSKL 333 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 301 93 94 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 34 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET 2 GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ 122 242 62 182 ઠે 셤 g 셤 셤 유 ð ઠે ઠે ò

TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346

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87 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG 146
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                                                                                                                                                                                                                                                                                                                                                                                                  human; enzyme; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate agent as modulator of function of a targ protein for treating cellular proliferation disorders by adding candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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               TRLLQDSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 378
                                                                                                                                                                                                                                                                                                                                                 Human kinesin-like DNA binding protein (KID) (SeqID 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                          ADC23340 standard; protein; 512
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20-JUN-2000; 2000US-00597292.
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                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; ADC23339.
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The invention relates to human microtubble motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, modulators of the target protein, modulators of the target concer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for careening for modulators of motor proteins useful for treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac proliferation disorders and inflammation, for treating disorders hypertrophy, immune disorders and inflammation, for treating disorders
                                    206
                                                                              241
                                                                                                    267 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVFYRDSKL 326
181
                                                                                                                                                         242 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNOGLPRVPYRDSKL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                                                            LIPGLSQKPISSPADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
VIPRALMDLLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
                     302 TRLLODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEVIN 346
                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microtubule motor protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                           ADQ60230 standard; protein; 512
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET

Best Local Similarity 100. Matches 345; Conservative

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LKYQFDAFYGERSTQQDIXAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG

N-PSDB; ADQ09241

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                                                                                                                                                                                                                                 98
associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not appear to be the case.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; energineuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                                                                                                                                                                                                                                                          LKYQFDAFYGERSTQQDIYAGSVQFILRHLLEGQNASVLAYGFTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                                                                         GRCRLSKIGATRRPPPARVRVAVRLRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                                                                                                                     87 LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
                                                                                                                                                                                                                                                                                                                                     147 VIPRALMDLLQLTREEGAEGREWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thanatos-associated protein; THAP; THAP responsive gene; THAP family;
                                                                                                                                                                            0; Gaps
                                                                                                                                                 Length 512;
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                                                                                                                                               99.7%; Score 1763; DB 8; L
100.0%; Pred. No. 7.4e-173;
Ative 0; Mismatches 0;
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                           Query Match . 99.79
Best Local Similarity 100.0
Matches 345; Conservative
                                                                                                                     512 AA;
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The present invention describes a method for modulating the expression of a thanaros (death)-associated protein (THAB) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repression the PTHAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/chemokine complex; (2) a pharmaceutical composition comprising a THAP/chemokine a compising a transcription factor decy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment; (3) a renormality of a THAP responsive element; (4) a cell comprising a transcription factor decy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment; (3) a vector packaging cell line complex; (5) a vector packaging cell line complex; (6) a vector packaging cell line complex; (7) a method of constructing a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide; (8) methods of instructions associated with a condition mediated by a THAP/chemokine complex; (6) methods of instructions and condition mediated by a THAP/chemokine into the nucleus; (10) methods for reducing the symptoms associated with a condition mediated by a THAP/chemokine or a transcriptional resulting from the associated with ranscriptional resulting from the condition associated with ranscriptional regulated in an individual; or symptoms associated with ranscriptional represses a THAP-family polypeptide in an individual; (11) a vector described above or that expresses a THAP-family polypeptide that does not bind to a chemokine or less than the animance of composition and estectable product; (12) a genetically mediated b
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                                        Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the
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100.0%; Pred. No. 1.1e-172;
ive 0; Mismatches 0;
                                                                                                                                                         Example 47; SEQ ID NO 425; 612pp; English
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Matches 345; Conservative
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Clouaire

Roussigne M,

Girard J, Amalric F, WPI; 2004-525034/50

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122 VIPRALMDLLQLTREEGAEGREWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 REGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKL 303
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                                                                                                                                                           4 GRCELSKIGATRRPPPARVRVAVRIRPFVDGTAGASDPPCVRGMDSCSLEIANWRNHQET
                                                                                                                             LKYQFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPG
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                                                                                                                                                                                                                                                                                                                                       LIPGLSQKPISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ
                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 40128.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; gastrointestinal; pene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AARISS66 to AARISSOS encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AABSSOS to AABS7302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, candiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS to AAFISSOS ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING AFISSOS ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING ABSENTING AB
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Human prostate cancer antigen protein sequence SEQ ID NO:1228.
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Pred. No. 6.8e-172;
; Mismatches 2;
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Best Local Similarity 99.4
Matches 343; Conservative
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N-PSDB; AAF15853.
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i1. .25
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                                                                                                al Similarity
132; Conserv
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Best Local &
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                                                                                                                                                                                                        233 RERLAPFROREGKLYLIDLAGSEDNRRTGNKGLRLKESGAINTSLFVLGKVVDALNQGLP 292
                                                                                                           HOETLKYOFDAFYGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTM---L 114
                                                                                                                                                   GSPEQPGVIPRALMDL-LQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVI 173
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                                                                    TRRP-----PPARVRVAVRLRPFVDGTAGASDPPCV-----RGMDSCSLEIANW--RN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                  CD-TETNTIKVGKLNLIDIAGSERQSKTGASAERLKEASKINLALSSLGNVISALAESSP
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                                                                                                                                                                                                                                                                                        293 HVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYASRAKSIQN 346
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                             784;
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                             Length
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      human; gene therapy; diagnostic marker; pharmaceutical
                                                126;
                             DB 4;
                          31.6%; Score 559.5; DB 4
39.8%; Pred. No. 4.4e-48;
ive 56; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein of the invention SEQ ID NO:2692
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                                    Local Similario,
nes 141, Conservative
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Seki N, Yoshikawa T,
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       Sequence 784 AA;
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                          Query Match
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detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural and cytoskeleton-associated polypeptide, SCAP, cell proliferative disorder; cancer, atherosclerosis, viral infection, HIV, neurological disorder; Parkinson's disease, Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                      19 RVRVAVRLRPP--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQFDAF
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                                                                                                                                                                                                                                 31.6%; Score 559; DB 7;
38.9%; Pred. No. 2.8e-48;
tive 70; Mismatches 121
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"potential phosphorylation site"
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790
/note= "potential phosphorylation site"
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'note = kinesin motor domain
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The present sequence represents a structural and cytoskeleton-associated polypeptide (SCAP). The SCAP polypeptides and polymucleotides of the invention are useful for diagnosing, preventing or treating diseases or conditions associated with aberrant expression of SCAP, such as cell proliferative disorders (e.g. cancer or atherosclerosis), viral infections (e.g. HIV) or neurological disorders (e.g. Parkinson's disease, Allakaimer's disease or stroke). These may also be used for assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are also useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. 70 YGERSTQQDIYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTMLGSPEQPGVIPRALMD 129 Swarnakar A, Ho A, Hafalia AJA, Emerling BM, Ison CH, Nguyen DB; Chien D, Lu DAM, Yang YG, Yue H, Murage J, Griffin JA, Burrill JD; Wang JT, Marquis JP, Blake JJ, Chawla NK, Lee S, Becha SD, Lee SY; Richardson TW, Bhatia UG, Zheng W, Sprague WW, Tang YT, Azimzai Y; 11 QLMVALRVRPISVABLEEGATLIAHKVDEQMVVLMDPWEDPDDILRAHRSREKSYLFDVA 19 RVRVAVRLRPF--VDGTAGAS-----DPPCVRGMDSCSLEIANWRNHQETLK-YQFDAF Gaps New human structural and cytoskeleton-associated proteins and polynucleotides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cancer, atherosclerosis, HIV or stroke. 16; 31.6%; Score 559; DB 8; Length 998; 38.9%; Pred. No. 7.1e-48; ive 70; Mismatches 121; Indels /note= "potential phosphorylation site" phosphorylation site" 'note= "potential phosphorylation site" 'note= "potential phosphorylation site" "potential phosphorylation site" /note= "potential phosphorylation site" "potential glycosylation site" phosphorylation Claim 1; Page 150-152; 205pp; English. "potential "potential 27-SEP-2002; 2002US-0414227P. 18-NOV-2002; 2002US-0427594P. 07-FEB-2003; 2003US-0445724P. 07-MAR-2003; 2003US-0453277P. 24-SEP-2003; 2003WO-US030198 31.69 Best Local Similarity 38.99 Matches 132; Conservative /note= /note= 'note= 'note= (INCY-) INCYTE CORP. WPI; 2004-305155/28. N-PSDB; ADO44181. Sequence 998 AA; WO2004029205-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 08-APR-2004. 셤 8 ò

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Claim 11; Fig 3; 66pp; English.

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                                                                                                                                           248 MIDLAGSERASQTQNRGQRMKEGAHINRSLLALGNCINALSDKGSNKYINYRDSKLTRLL 307
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LLQLTREEGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSQK 189
                                                                                                                  LIDLAGSEDNRRIGNKGLRLKESGAINTSLFVLGKVVDAL-NGGLPR-VPYRDSKLTRLL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222. .229
//abel= SwitchI motif
//oce= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
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/note= "Responsible for sensing of the gamma phosphate
and initiating the conformational change between ATP and
ADP bound forms of the enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                     Kinesin, motor protein; HsKip3d, cytostatic; immunosuppressive; antiarthritic; antinflammatory; vulnerary; microtubule; inflammation, cardiac hypertrophy, cellular proliferation disease; hyperplasia; restenosis; cancer; solid tumour; carcinoma; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; surgery; angioplasty; nanotechnology; GeneChip array; expression monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Interacts with the adenine ring of ATP to form
                 190 PISSFADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQ--REGKLY
                                                                                                                                                                                                                                                                                                                                                                        Novel human kinesin motor protein, HsKip3d motor domain.
                                                                                                                                                                          ODSLGGSAHSILIANIAPERRFYLDTVSALNFAARSKEV 344
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KDSLGGNSRTVMIAHISPASSAFEESRNTLTYAGRAKNI 346
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113. .120
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N-PSDB; ABK10348.
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The invention describes an isolated novel human microtubule motor protein (I) is useful for screening modulators of HsKip3d. The method comprises contacting (I) with a candidate agent in a test and control concentration, and assaying for the level of HsKip3d activity, where the HsKip3d activity between the level of HsKip3d activity, and where a change in activity between the test and control concentration indicates a modulator. A composition containing (I) is useful in the treatment of inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. inflammation, cardiac hypertrophy, cellular proliferation diseases e.g. byperplasias, reseneousls, cancer, including solid tumours of skin, bream, lung, heart, bone, genitourinary tract, liver, nervous system, adrenal glands, haematologic, gynaecological and testicular carcinomas, autofimmune disease, arthritis, graft rejection, inflammatory bowel disease, proliferation induced after medical procedures, such as surgery, angioplasty. The motor domains may also be used in nanotechnological applications, and polymuclectides encoding the proteins is further useful for inclusion on GeneChip (RIM) array or for use in entor montor in expression monitoring. This is the amino acid sequence of the novel human motor in monitoring. This is the amino acid sequence of the novel human motor in the method of the
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Best Local Similarity 39.7%; Pred. No. 6.9e-48;
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US-09-724-224-5
Sequence 5, Application US/09724224
Fatent No. 6387644
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 638764el motor proteins and methods for TITLE OF INVENTION: their use
CURRENT APPLICATION NUMBER: US/09/724,224
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 09/597,292
FRIOR FILING DATE: 2000-6-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1041
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   Similarity
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GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAAG 900
                                                                                   GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG
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                 841 GGCAAAGTGGTAGATGCGCTGAATCAGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
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Patent No. 6762043

GENERAL INFORMATION:

I GENERAL INFORMATION:

I TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/10/093,317

CURRENT FILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Human
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                   Sequence 7, Application US/09724224

Sequence 7, Application US/09724224

Retent No. 6387644

GENERAL INFORMATION:

APPLICANT: Berand, Christophe

TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use

FILE REPERENCE: 1044

CURRENT APPLICATION NUMBER: US/09/724,224

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR PLING DATE: 2000-6-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 1464
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99.8%; Score 1038.4; DB 3; Length 1464;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1039; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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Best Local Similarity
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; ORGANISM: Human
US-09-724-224-1
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| Patent No. 6387644
| GAREAL INFORMATION:
| APPLICAMY: Beraud, Christophe
| TITLE OF INVENTION: No. 6387644el motor proteins and methods for TITLE OF INVENTION: their use
| FILE REPERENCE: 1044
| CURRENT APPLICATION NUMBER: US/09/724,224
| CURRENT PILING DATE: 2000-11-28
| PRIOR APPLICATION NUMBER: 09/597,292
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SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. v,
... 0; Mismatches
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TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/093,317
CURRENT FILING DATE: 2002-03-06
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
                                                             Sequence 1, Application US/10093317
Patent No. 6762043
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1038; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 1115
                                             -10-093-317-1
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  Length 1538;
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  Query Match 99.5%; Score 1035.4; DB 4; Best Local Similarity 99.9%; Pred. No. 9.9e-315; Matches 1036; Conservative 0; Mismatches 1; I
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                                AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCCAG
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US-10-093-317-3

Sequence 3, Application US/10093317

Factor No. 6762043

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: No. 6762043el motor prote

TITLE OF INVENTION: their use

FILE REFERENCE: 1044

CURRENT APPLICATION NUMBER: US/10/093,317

CURRENT FILING DATE: 2002-03-06

FRIOR APPLICATION NUMBER: US/10/093,317

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1538

TYPE: DNA

TYPE: DNA

GGANISM: Human

US-10-093-317-3
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                                                             CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGGTCAACCAGCGCTCCTCCCGC
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Best Local Similarity 51.2%; Pred. No. 1.2e-32;
Matches 437; Conservative 0; Mismatches 389; Indels
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; Sequence 6, Application US/09883096
; Patent No. 6680369;
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Craven, Andrew
; APPLICANT: Taxen, Andrew
; APPLICANT: Patel, Umesh A.;
; APPLICANT: Davies, Ratherine A.;
; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METI;
; FILE REFERENCE: 020552-001410US
; CURRENT APPLICATION NUMBER: US/09/883,096
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; SOFTWARE: PatentIn Ver: 2.1
; SEQ ID NO 6
; LENGTH: 1152
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ORGANISM: Artificial Sequence
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Pred. No. 9.9e-315;
0; Mismatches 1; Indels 0;
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Best Local Similarity 99.9%;
Matches 1036; Conservative
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ORGANISM: Human
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                                                                                                                                                                                          OTHER INFORMATION: Nucleic acid sequence of human kinesin motor OTHER INFORMATION: protein gene HsKip3a (Figure 1). OTHER INFORMATION: Description of Artificial Sequence: HsKip3a gene.
                                                                                                                                                                                                                                                                                                                                                                                     Indels.
                                                                                                                                                                                                                                                                                                                                Score 136.6; DB 4;
Pred. No. 2.4e-32;
0; Mismatches 389;
                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                Query Match
13.1%;
Best Local Similarity 51.2%;
Matches 437; Conservative
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     NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 4108
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                                                                                                                  Sequence 1, Application US/09883096

Patent No. 6680369

GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Tu, Ming
APPLICANT: Tu, Ming
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 202052-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT APPLICATION NUMBER: US/09/683,096
CURRENT APPLICATION NUMBER: US 09/594,655

PRIOR FILING DATE: 2000-06-15
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Patent No. 638841

GENERAL INFORMATION:

APPLICANT: Berand, Christophe

APPLICANT: Bread, Richard

TITLE OF INVENTION: No. 636841el motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: L1045

CURRENT PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-07-21

NUMBER: OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc feature
LOCATION: (472)... (495)
OTHER INFORMATION: n = a, c, t, or
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Best Local Similarity 50.1
Matches 429; Conservative
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Patent No. 6294371
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6294371e1 motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1045
CURRENT APPLICATION NUMBER: US/09/621,233
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASESEQ for Windows Version 4.0
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12.3%; Score 127.8; DB 3; Length 897;
Best Local Similarity 50.1%; Pred. No. 5.9e-30;
Matches 429; Conservative 0; Mismatches 356; Indels 72
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; Sequence 1, Application US/10090695
; Patent No. 6664072
; GAPERRAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 664072el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1045
; CURRENT APPLICATION NUMBER: US/10/090,695
; CURRENT APPLICATION NUMBER: 09/621,233
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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Patent No. 6391573

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard

ITILE OF INVENTION: No. 6391573e1 motor proteins and methods for

TILLE OF INVENTION: Heir use

FILE REFERENCE: 1045

CURRENT APPLICATION: NUMBER: US/09/724,516

CURRENT FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 09/621,233

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc feature
LOCATION: (472)...(495)
OTHER INFORMATION: n = a,
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LENGTH: 897
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964 GCCCCTGAGAGACGCTTCTACCTAGACACACTCCGCACTCAACTTTGCTGCCAGGTCC 1023
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                                                                                                                                                                                                                                                                                 Score 127.8; DB 4; Length 897;
Pred. No. 5.9e-30;
0; Mismatches 356; Indels 72;
                                                                | FEATURE: | NAME/KEY: misc feature | LOCATION: (472)...(495) | LOCATION: (472)...(495) | LOCATION: 0.0000.695-1
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Best Local Similarity 50.1%;
Matches 429; Conservative 0
TYPE: DNA
ORGANISM: Human
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AF267850  AD2769850  AD2769891  AC023331  AC023331  AC0233131  AC0333125  AC123480  AC123480  AC123480  AC123480  AC12253	ENTS  DNA line 544.  their use 1002;	100.0%;   Score 1041;   DB 6;   Length 1041;
20 438 6 42.1 2593 5 AF267850 21 438.6 42.1 2661 5 XLA249840 22 438.6 42.1 2661 5 KLA249840 23 438.6 42.1 2781 5 BC070549 23 438.6 42.1 2781 5 BC070549 24 355.4 34.1 174007 9 AC02331 25 352.2 33.8 336 9 AB0173352 27 346.4 33.3 105485 9 HUAC02301 28 378.4 26.7 68916 2 AC131376 28 32 265.5 229504 2 AC123480 26 25.5 22896 2 AC123480 26 25.5 22896 2 AC123480 26 25.5 226601 10 AC1222853 26 25.5 226601 10 AC1222853 26 25.5 226601 2 AC123460 26 32 265.2 19997 10 AC1222863 36 184.6 17.7 2095 6 AX033125 37 184.6 17.7 2095 6 AX033125 38 153.2 14.7 146415 5 AL929469 39 153.2 14.7 146415 5 AL929469 41 145.8 14.0 435 5 AC092563 44 136.6 13.1 13.5 183586	136.6 13.1 4108 6 AR45416  14 AR210054 1041  10N Sequence 5 from patent US 638  N AR210054 GI:21512185.  S Unknown.  ISM Unknown.  ISM Unknown.  ICE 1 (bases 1 to 1041)  RS Beraud, C.  RS Beraud, C.  RA Patent: US 6387644-A 5 14-MA;  Location/Qualifiers  1. 1041  AR210054 1041)  RS Beraud, C.  AR210054 1041)  RS Beraud, C.  AR210054 1041)  RS Beraud, C.  AR210054 1041)  RS Beraud, C.  AR210054 1041)  RS Beraud, C.  AR210054 1041)  RS Beraud, C.  AR387 1041)  RA Patent: US 6387644-A 5 14-MA;  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041  AR388 1041 1041	Ouery Match Best Local Similarity 100.0%; Pred. No. 1.9 Matches 1041; Conservative 0; Mismatches Oy 1 ATGGGTGGTGGGTAAGCAAGATTGGAGGTG Oy 61 AGGGTGGTGGCTAAGCAAGATTGGAGGTG Oy 121 TGTGGGGTGGCTGTGGGCTTTGTGGATG Oy 121 TGTGGGGGGTGGGGTTGGGGTGGGTTGGATGGATGGATG
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5.1.6 Compugen Ltd Search time 4600.34 Seconds (without alignments) 10701.074 Million cell updates/secccaaggaggtgatcaattga 1041 esidues meters: 9053458	summaries  summaries  results predicted by chance to have a l to the score of the result being printed, of the total score distribution.  SUMMARIES	AR210054 Sequence AR210055 Sequence AR210055 Sequence AR210053 Sequence BR007259 Homo sapi BR007898 Synthetic AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Sequence AR304057 Mus muscu AC101919 Mus muscu AC101919 Mus muscu AC101109 Mus muscu AC101108 Mus muscu AC101108 Mus muscu AC102127 Mus muscu AC102127 Mus muscu AC102127 Mus muscu AC102127 Mus muscu AC102137 Xenopus I BC043733 Xenopus I BC043731 Xenopus I
GenCore version 5.  Bearch, using sw model  mber 9, 2004, 19:47:28; S  1070  0-797-893-5  3991cgctgtcggctaag  IITY NUC  0.10-0, Gapext 1.0  729 seqs, 23644849745 resid  satisfying chosen paramete  1: 2000000000	timum Match of timum Match 10 string first 4, string first 4, string first 4, gb_ba:* gb_btg:* gb_pt:*	Query  Match Length DB ID  100.0 1041 6 AR210055 99.8 1464 6 AR210055 99.7 1115 6 AR210055 99.5 1998 9 BT007259 99.5 2097 9 AR010457 99.5 217 9 BC028155 99.5 217 9 BC028155 99.5 2184 9 BC004352 74.2 2086 10 BC003427 65.1 151041 2 AC101919 65.1 164759 10 AC101752 65.1 164759 10 AC101752 65.1 164759 10 AC10127 44.4 2756 5 BC043733 43.7 2563 5 BC043733 43.7 2564 5 BC043737
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99.8%: Score 1038.4	Indels	Oy 1 ATGGGTGTCGCTAAGCAAATTGGAGCTACTCGTCGACCTCCAGCTCGCGTA 60	Qy         61 AGGGTGGCTGTGCGGCCATTTGTGGAACAGCAGCAAGCAA	Qy         121         TGTGTGCGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACGGAG         180	QY         181 ACTCTCAAATACCAGTITGATGCCTTCTATGGGAGAGGAGTACTCAGCAGACATCTAT         240           Db         181 ACTCTCAAATACCAGTITGATGCCTTCTATGGGGAGAGTACTCAGCAGGACATCTAT         240	Qy         241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGAATGCCAGTGTGCTT         300           bb         241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCAGAATGCCAGTGTGCTT         300	QY         301 GCCTATGGACCCACAGGAGCTGGGAAGACACCACACACTGGGCAGCCCAGAGCAACCT         360           Db         301 GCCTATGGACCCACAGGAGCTGGGAAGACACACACAATGCTGGGCAGCCCAGAGCAACCT         360	OY 361 GGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGAGGAGGTGCCGAG 420	QY         421 GGCCGGCCATGGGCCCTTTCTGTCCATGTCTTACCTAGAGATCTACCAGGGAAAGGTA 480	QY         481         TTAGACCTCCTGGTCGCTTCGGGAGCCCTGGTAATCCGAGAAGACTGCCGGGGGAAT         540           DD         481         TTAGACCTCCTGGTCTTCGGGAGCCCTGCTTAATCCGAGAAGACTGCCGGGGGAAT         540	QY         541 ATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCAC 600           Db         541 ATCCTGATTCCGGGTCTCTCCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCAC 600	QY         601         TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGTCAACCAGCGCTCCTCC         660         TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCC         660         TTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCGGGCTCAACCAGCGCTCCTCC         660	OY 661 CGCAGTCATGCTCCTCGTCAAGTGGACCAGGGGGAAAGTTTGGCCCCATTTGG 720	Oy 721 CAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTGAGGACAACCGGCGCACA 780	841	OY 901 CTCACTGGCTATTGCAGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC 960	QY         961 ATTGCCCCTGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGG 1020
Db 241 GCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTT 300 Qy 301 GCTATGGACCCAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCT 360	BAGCAACCT 3	QY 361 GGGGTGATCCCGCGGGGCTCTCATGGACCTCCTGCAGCAAGGAGGGGGGGG	Oy 421 GGCCGGCCATGGCCATTCTCTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTA 480	Oy 481 TTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAAT 540	OY 541 APCETGATTCEGGGTETTCECCAGAAGCECAPAGTAGETTTGGTGATTTTGAGGGGCC 600	Oy 601 TICCTGCCAGCCAGICGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCC 660	OY 661 CGCAGTCATGCTCTCGTCAAGGTGGACCAGCGGAACGTTTGGCCCCATTTCGC 720	Oy         721         CAGCGAGAGAAAACTCTACCTGATTGACTTGGGTCAGAGACAACGGGGCACA         780           bb         721         CAGCGAGAGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACGGGGCACA         780	OY 781 GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG 840	OY 841 GGCAAAGTGGTAGATGGGTGAATCAGGCCTCCTCGTGTACCTTATCGGGACGGAG 900	OY 901 CTCACTCGCCTATTGCAGGACTCTCTCGGTGGCTCACCCACAGTATCCTTATTGCCAAC 960	OY 961 ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCTACTTTGCTGCCAGG 1020	Oy 1021 TCCAAGGAGGTGATCAATTGA 1041	RESULT 2 AR210055 LOCUS AR210055 LOCUS AR210055 DEFINITION Sequence 7 from patent US 6387644. ACCESSION AR210055 VERSION AR210055		AUTHORS Beraud, C. TITLE Motor proteins and methods for their use JOURNAL Patent: US 638764-A 7 14-WAY-2002; FRATURES	rae

664 AGTCATGCTGTGCTCCTG 738 AGTCATGCTGTGCTCCTG 724 CGAGAGGGAAAACTCTACC 784 AACAGGGGAAAACTCTACC 784 AACAGGGCTTCGGCTA 858 AACAGGGCTTCGGCTG 844 AAAGTGGTAGATGCGCTG 904 ACTCGCCTATTGCAGGCT 904 ACTCGCCTATTGCAGGCT 904 ACTCGCCTATTGCAGGCT 905 ACTCGCCTATTGCAGGCT 906 ACTCGCCTATTGCAGGCT 907 BCCCCTGAGAGCCTTC 908 GCCCCTGAGAGCCTTC 909 ACTCGCCTATTGCAGGCT 909 ACTCGCCTATTGCAGGCT 909 ACTCGCCTATTGCAGGCT 900 ACTCGCCTATTGCAGGCT 900 ACTCGCCTATTGCAGGCT 901 ACTCGCCTATTGCAGGCT 901 ACTCGCCTATTGCAGGCT 902 ACTCGCCTATTGCAGGCT 903 ACTCGCCTATTGCAGGCT 903 ACTCGCCTAGAGACGCTTC 904 ACTCGCCTAGAGACGCTTC 904 ACTCGCCTAGAGACGCTTC 905 ACTCGCCTAGAGACGCTTC 906 ACTCGCCTAGAGACGCTTC 907 ACTCGCCTAGAGACCTTCTCTCTCTCTCTCTCTCTCTCTC	Op         1024 AAGGAGGTGATCAATTGA 1041           Db         1098 AAGGAGGTGATCAATTGA 1115           RESULT 4         AR210053           AR210053         1538 bp         DNA           LOCUS         AR210053         167644.           DEFINITION         AR210053         16721512183           ACCESSION         AR210053.1 G1:21512183           VERSION         AR210053.1 G1:21512183           KEYMORDS         Unknown.           ORGANISM         Unclassified.           Unclassified.         Unclassified.           AUTHORS         Beraud,C.           AUTHORS         Accation/Qualifiers           JOURNAL         Patent: US 6387644-A 3 14-MAY-2002;           FRATURES         Location/Qualifiers           JOURNAL         Accation/Qualifiers           Accation/Lype="unassigned">/ Anglobal           Amol_Lype="unassigned">/ Anglobal	Query Match         99.5%;         Score 1035.4;         DB 6;         Length 1538;           Best Local Similarity         99.9%;         Pred. No. 6.1e-266;         0;         Gaps         0;           Matches 1036;         Conservative         0;         Mismatches         1;         Indels         0;         Gaps         0;           Qy         4 GGTCGCTGTCGCCTAAGCAAGATTGGAGTACTCGTCGTCCACCTCCAGCTCGCGTAAGG         137         0<
Cy         1021 TCCAAGGAGGTGATCAATTG 1040           Db         1021 TCCAAGGAGGTGATCAATTG 1040           RESULT 3	Query Match         99.7%; Score 1038; DB 6; Length 1115;           Best Local Similarity 100.0%; Pred. No. 1.2e-266;         Additional Similarity 100.0%; Pred. No. 1.2e-266;           Qy         4 GGTCGCTGTCGGCTAAGCAAGTTGAGCTACTCGTCGTCCACCTCCAGCTCGCTAAGG 63           Db         78 GGTCGCTGTCGGCTAAGCAAGTTGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG 137           Qy         64 GTCGCTGTCGGCTAAGCAAGTATTGGAGCTACTCGTCCACCTCCAGCTCGCGTAAGG 137           Qy         64 GTCGCTGTGCGACTCGGGCCATTTGTGGAACAGCGGGAGCAGTCATCCCCCTTT 197           Db         138 GTGGCTGTGCGACTCCGGCCATTTGTGGAACAGCGGGAGCAATCCCCCCTTT 197           Qy         124 GTGCGGGCATGGACGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT 183           Db         198 GTGCGGGCATGGACGCTCTCTAGGGAATTGCTAACTGGAGGAACCACCAGGAGACT 257           Qy         184 CTCAAATACCAGTTTGATGCTTCTATGGGAGAGGAGATCCAGCAGAACTCTATGCA 243           Db         258 CTCAAATACCAGTTTGATGCTTCTATGGGAGAGGAGAACTCAGCAGAACTTATGCA 317           Qy         244 GGTTCAGTCAGCCCTTCTAAGGACTTGCTGGAAGGGAGAATGCTTGCT	CCTGGG CCTGGG CCTGGG GAGGGC GAGGGC GAGTTA ANTATC ANTATC CACTTC CACTTC CACTTC CACTTC CACTTC

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Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms; with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNM-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATC' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Incation/Qualifiers
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, W., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phellan, M. and Farmer, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAAGGSTQQRRREMAAASAAAISGAGRCRLSKIGATRRPPPARV
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GSEDNRRTGWKGLRLKESGAINTSLFVLGKVVDALNQGLPRVPYRDSKLTRLLQDSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSAHSILIANIAPERREYLDTVSALNPAARSKEVINRPETNESLOPHALGPVKLSGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH5alpha T1 resistant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.5%; Score 1035.4; DB 9.11 prity 99.9%; Pred. No. 6.1e-266; Conservative 0; Mismatches 1;
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1 (Dases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundânya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Choning of human full-length CDSs in BD Creator(TM) System Donor
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HGPFSQVEDLERVEGITGKQWESFLKANILGLAAGGRCGASL"
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and Hindrill sites of the PDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before Hindlil site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
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/note="Mutations: 1997:Stop->Leu"
                                                                                                                                                                                                                                                                                                                                       /lab_host="DH5alpha T1 resistant"
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1 (bases 1 to 1998)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
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Unclassified.
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Beraud, C., Ohashi, C., Sakowicz, R., Vaisberg, E., Wood, K. and Human Kinesins and methods of producing and purifying human kinesins and methods of producing and purifying human kinesins
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Location/Qualifiers
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/mol_type="genomic DNA"
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Sequence 34 from patent US 6544766.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Tokai-Nishizumi, N. and Edamasu, M.

Tokai-Nishizumi, N. and Edamasu, M.

Direct Submission

Tokyo, The Institute of Medical Science, Department of Oncology;

4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

(E-mail:tokai@hgc.ims.u-tokyo.ac.jp, Tel:03-5449-5302,

Fax:03-5449-5413)

D38751:Submitted (02-Nov-1994)

Sequence updated (25-Feb-1999).

Location/Qualifiers

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PTWLRPLSHRTVTGAKPLKKAVWHDLOLIOGOAASPNAEIHILKNKGRKRKLESLDAL
EPPERKAEDWELQISPPELLAHGROKILDLINBGSARDLIRSLQRIGPKKAQLIVGWREL
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                                                                     AB017430.2 GI:4519442
Kid; Kinesin-like DNA binding protein; kinesin family
Homo sapiens (human)
Homo sapiens
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             Strausberg L.U., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer (C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrisues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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Contact: MGC help desk
Email: cgapbs.ra@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgirinh.gov
Contact: nisc.mgc@nhgirinh.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Banjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Cana,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
TBurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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TITLE
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                                                                                                                                                                                                                                                     ADFERHFLPASRNRTVGATRLNQRSSRSHAVILJVKVDQRERLAPFRQREGKLYLIDLA
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                                                                                                                                                                                                                                                                                                                                                                     ASGGSGGAPLLSTPKRERMVIMKTVEEKDLEÏERLKTÄQKELEAKMLAQKAEEKENHC
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EPEEKAEDCWELQISPELLAHGRQKILDLLNEGSARDLRSLQRIGPKKAQLIVGWREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 1035.4; DB 9; Length 2117; 99.9%; Pred. No. 6.1e-266; ative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGPFSQVEDLERVEGITGKQMESFLKANILGLAAGQRCGAS
  member 22"
/product="kinesin family
/protein_id="AAH28155.1'
/db_xref="G1:20380447"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: f Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="Locusid:3835"
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BGAEGRPWALSVTMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILIPGLSGKPISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADFERHFLPASRNRTVGATRLNQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLA
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GSAHS ILIANIAPERFYLDTVSAINFARSKEVINRPFTNESLQPHALGPVKLSQKE
LLGPPEAKRARGPEEEEIGSPEPMAAPASASQKLSPLQKLSSNDPAMLERLLSLDRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASQGSQGAPLLSTPKRERMVLMKTVEEKDLEİERLKTKQKELEAKMLAQKAEEKENHC
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                                    info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilaa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="KIF22"
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Pred. No: 6.1e-266;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Lung, small cell carcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="MGC:1573 IMAGE:3535435"
             BC Cancer Agency, Vancouver, BC, Canada
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg N.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F., Diatchenko, L., Maruslana, K., Earmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosk, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Chein, J.E., Jones, S.J. and Marra, M.A., Chein, J. R., Jones, S.J. and Marra, M.A., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L. J., L
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22, mRNA (cDNA clone MGC:1573
                                                                                                       843
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
921 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTATCGTGACGACAGCAGCTC
                                                                                                                                                                                                                                                                                                                                                         ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
                                                                                                                                                                                                                                                                                                                                                                                                     981 ACTCGCCTATTGCAGGACTCTCTGGGGGGCTCAGCCCACAGTATCCTTATTGCCAACATT
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                                                                                                                                                                                                                              844 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCTCGTGTACCTTATCGGGACAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens kinesin family member
IMAGE:3535435), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101 AAGGAGGTGATCAATCG 1117
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BC004352.1 GI:13279307
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Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heieh, F., Diacchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N.A., Peters, G. J., Abramson, R. D., Mulahy, S. J., Bosak, S. A., McEwan, P. J., Malek, J. A., Gunaratne, P. H., Richards, S. Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Miting, M., Madan, A., Rodrigues, S., Sanchez, M., Miting, M., Madan, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Schmutz, J., Schmutz, D. Schmutz, J., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut, J. B., Schmut,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="MG1:109233"
/translation="MSLRAKTCPQRREMASATSGPGRCVSKGGLGRRPPLARVRVAVR
LRPPMDGETEAKELPCVRAIDSCSLEVANWKKYQETLKYQFDAFYGEKSTQQEVYYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 5 Row: m Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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protein_id="AAH03427.1"
/db_ref="G1:13097360"
/db_xref="LocusID:110033"
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/clone="MGC:6456 IMAGE:2615715"
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/db_xref="LocusID:110033"
/db_xref="MGI:109233"
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/strain="FVB/N"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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                                                                                                                                       TATGGACCCACAGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG
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AUTHORS
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	RESULT 12 AC101919 AC101919 BURN BURNELON MUS musculus clone RP24-158A6, WORKING DRAFT SEQUENCE, 4 unordered pleces: AC101919 AC1010101 AC101919 AC101910 AC10101 A	TITLE Direct Submission J. Zembek, L., Zimmer, A. and Zody, M. Direct Submission Journal Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA REFERENCE BITTER, B., Nubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukhgaller, B., Camarta, J., Chang, J., Choepel, Y., Collymore, A., Cock, A., Cock, P., Cortum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Hagopian, D., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabtit, R., MacLean, C., Macdonald, P., Major, J., Malnay, T., Mathews, C., McCatthy, M., Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Peterson, K., Phunkhang, P., Pierre, N.,
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VQPILRHLLEGONASVLAYGPTGAGKTHTWLGSPEOPGGVIPPALMDLLOLAREESAEG RPMDVSVAMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILITGGLTQKEITTSFEDFEG RPMDVSVAMSYLEIYQEKVLDLLDPASGDLVIREDCRGNILITGGLTQKEITTSFEDFEG RFTGARGYTELKESGALINTSLFVLGKVVDRALNGCERELTPRESLGGSEDN RFTGANGGIRLKESGALINTSLFVLGKVVDALNGCEPRIPPERCREGKTLLLQDSLGGSAHS ILIANIAPERRFYQDTISALNFTARSKEVINRPFTNESLQPHALAPVKLGGKELIGPS RAKTAKGREBESTGARFARARASKGKLSLLGKLSMPRAHLENLLGSNGGS QGTPLLANPERGERNVLAKTAVVMPLQRIOKGKRESAKULAQEAPDPREKENTFTI LQPPASYSGTVAKPLKKAVVMPLQRIOKGRESSNQIOLLKKGFRKLEPSPRESEAVEK DEDVWRVQISPELLAHGRKKALLDLLNEGSARELRSLCRIGGKKAQLIVGWRELHGFFS GVEDLEQVEGISGKQVESFLKANLLSLAASGHSGPS"  Query Match Best Local Similarity 84.3%; Pred. No. 1.2e-195; Matches 870; Conservative 0; Mismatches 162; Indels 0; Gaps 0;		DD   622   GATCCCAGGCCTCACACAGAGCCCATCCTCTGAGCACTCCTC   681   606   GCCAGCCAGGCCTCTCTCAGCACTCCTCCCGCAG   665   6

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55399 GACTGGGGCAGGGAAGA - - CACACAATGTTGGGCAGCCCAGAACAGCCTGGAGTGATTCC
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                               65699 trgraraagcaagcaaccartcccrcrcrcrrcracracagaagraagcrcrar
                                                                                                                                                  252 GCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGGACC
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                                                                 GCGACTGCGGCCATTTGTGGATGGAACAGCGGGGGCAAGTGATCCCCCCTGTGTGCGGGG
                                                                                                                                 CATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACTCTCAAATA
                                                                                                                                                                                                 CCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCAGGTTCAGT
                                                                                                                                                                                                                                                                                                                            312 CACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATCCC
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   TCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGGGTGGCTGT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.18 33517: contig of 33517 bp in length 5518 33617; gap of 100 bp 6618 42736: contig of 9119 bp in length 42836; gap of 100 bp 837 84394: contig of 41558 bp in length 8195 84494; gap of 100 bp 6785 151041: contig of 66547 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L17745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment
clone end:876
vector_side:left"
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Locus

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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., O'Ilver, J., Peterson, R., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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          fagopian, D., Hagos, B., Hall, J., Horton, L.,
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Web site: http://www-seq.wi.mit.edu
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4202. .4363
/rpt_family="Lx7"
4529. .4765
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/rpt_family="AT_rich"
2115. .2157
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1673. .3731
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252. .3420
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complement(8512..859)
/rpt_family="MLT11"
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732. .3911
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1000. .4180
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464. .3588
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605. .3666
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8445. .8509
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Direct Submission

Direct Submission

Submitted (13-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 164759)

Birren, B., Wusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chhang, J., Choepel, Y., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gadgan, L., Gardam, L., Granders, P., Ritzderald, M., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Hagopian, D., Hagos, B., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liu, X., Liu, A., Mabbitt, R., Machens, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mahow, C., Micol, W., Minora, T., Minora, T., Minora, T., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schuuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, W., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wann, D., Young, G., Zainoun, V., Zembek, L., Zimber, R., and Zody, M., Direct, Submission
                                                                  AC101752 164759 bp DNA linear ROD 23-APR-2004
Mus musculus chromosome 1, clone RP24-344C18, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (184759)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chappel,Y., Collymore,A., Cook,P., Corum,B., DeArellano,K., Diaz,J.S., Docley,K., Dorris,L., Erickson,J., Raro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Plerre,N., Hafez,N.,
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 1, clone RP24-344C18
                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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                                                                      145871 ACAGCCCATACTAAGGAACTTGCTGGAAGGCAGAGAATGCCAGTGTACTTGCCTATGGACC 145812
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HTG; HTGS_PHASE1; HTGS_FULTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                              145811 GACTGGGGCAGGBAGA--CACACAATGTTGGGCAGCCCCAGAACAGCCTGGAGTGATTCC
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                                                                                                                                                                     GGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGGAATATCCTGATTCC
                                                                                                                                                                                                                                                                                                                                          552 GGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCTGCCAGC
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                                                         GCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGATGCCAGTGTGTGCTTGCCTATGGACC
                                                                                                               CACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGTGATCCC
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                                                   complement (11397. .17527)

rpt family="Lif"

complement (18235. .18777)
                                                                                                                                                                                 'rpt family="mull
lomplement (20386. .20639)
/rpt_family="Lx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="T-rich"
complement(30581. .34457)
rpt_family="L1 MM"
complement(34455. .35895)
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:omplement(36134. .36736)
                        complement (9800. .11396)
/rpt family="L1 MM"
complement (11397. .17527
                                                                                                                                                       family="RMER19A"
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1918. .22433
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8813. .28858
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9627. .30186
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1799. .21907
                                                                                                                                                                                                                                                                                                                                                                                                                                           family="AT_rich"
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27737. .27834
/rpt_family="MLT1H"
28328. .28506
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37958. .37986
/rpt_family="(GAA)n"
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24494. .24850
/rpt_family="L1_MM"
27139. .27166
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2733. .24486
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rpt_family="MLT1D"
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2591. 2221
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6749. .36920
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8775. .18890
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Best Local Similarity 80.0%;
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rnis record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                       1553 154450: contrig of 80450 bp in length 15451 154550: gap of 100 bp 1551 157808: contrig of 13250 bp in length 1570 15711: contrig of 13250 bp in length 15712 176311: contrig of 803 bp in length 15712 176311: gap of 100 bp 176311 gap of 100 bp 176312 233500: contrig of 5689 bp in length 1501 233500: gap of 100 bp 1601 241222: contrig of 7622 bp in length 1623 297639: contrig of 56317 bp in length. Location/Qualifiers
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                                                                                                             contig of 63747 bp in length gap of 100 bp contig of 10045 bp in length gap of 100 bp
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                                                                                                                                                                       Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Choepel, Y., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gorder, S., Gorder, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., McBwan, P., McKernan, K., Marquis, N., Matthews, C., Macdonald, P., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mandar, T., Narthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Nell, D., O'Nell, D., O'Nell, D., O'Nell, D., O'Nell, D., O'Nell, D., O'Nell, D., O'Shuyback, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Schupback, R., Standers, S., Schupback, R., Vola, R., Vola, R., Travers, M., Travis, N., Tragilio, J., Vassiliev, H., Viel, R., Vola, M., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N
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Burnett Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 297639)

Birren, B., Nusbaum, C., Lander E., Abouelleil, A., Allen, N.,

Bloom, T., Boqualavkiy, L., Boukhgalter, B., Camarata, J., Chang, J.,

Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,

Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,

Galagan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,

McCarthy, M., Meldrim, J., Meneus, L., Minoya, T., Mlenga, V.,

Murphy, T., Naylor, J., Naylor, J., Nanhova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nauyen, C., Nguyen, T., Nicol, R., Norbu, C.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,

Scomnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peeferson, K.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,

Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Feb 27, 2004 this sequence version replaced gi:31880232.

All repeats were identified using Repears
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Center: Whitehead Institute/MIT Center for Genome Research
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irren, B., Nusbaum, C. and Lander, E.
us musculus chromosome 1, clone RP24-275J1
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Submitted (10-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 1 (bases 1 to 196674)

Birrenh, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 196674)

Birrenh, B. Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Doode, S., Doodey, K., Dornis, L., Brickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Erickson, J., Faro, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lul, A., Mabbitt, R., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Manjor, J., Mihova, T., Manda, V., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Sewar, R., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Stohamer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zammer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zammer, A., Sumitra, A., Raine, R., Shane, R., Shane, R., Shane, R., Shane, R., Shane, R., Shane, R., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J., Shane, J.
                       Submitted (01-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 1, 2004 this sequence version replaced gi:46358225.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/MIT Center for Genome Research
Research, 320 Charles Street, Cambridge, MA 02141, USA
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/clone_lib="RPCI-23 Female Mouse BAC"
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Center clone name: 202 A 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 CTGAAAGATGTTTTTACCTGGATACAATCTCAGCATTAAACTTCACTGCTAGGTCCAAGG 162
                                                                                                                                                                                                                                                                                                                                                                                461 AAAACTCTACCTTATTGATTTGGCTGGTTCAGAGGACAACCGTCAGTCGCACAGGCAACC 402
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Birren, B., Nusbaum, C. and Lander, B.
Mus musculus chomosome 1, clone RP23-202A19
Unpublished
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
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Mus musculus chromosome 1, clone RP23-202A19, complete sequence.
AC102127
                                                   CAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGCAGTCATGC
                                                                                                                                                      672 TGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 TGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGGAGCAAGTGATCCCCCCTGTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 AGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 ACCCACAGAGGTGGGAAGACGCACACAATGCTGGGCAGCCC----AGAGCAACCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    665 GTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGC
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DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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/product= "KID protein"
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ABT40796
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Adg60241 Human KNS
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Ach44993 Human foo
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Ach91108 Human gen
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Listing first 45 summaries
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consistency that the states to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular consistency and also specifically, it refers to candidate agents that considers. Specifically, it refers to candidate agents that considers apable of modularing the activity of target proteins having motor of phosphate. Furthermore, this activity can be determined using or phosphate. Furthermore, this activity can be determined using considerate that identifies modulators of the target protein, which is a method that identifies modulators of the target protein, which is a considerate, can be used for the transmined cancer, hyperplasias, the statistic hypertrophy, incompassible that inflammatories. Accordingly, through gene therapy, they can be used for the transmined cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This colymucleotide sequence is human KID DNA (SeqID 5) encoding a full length can be used for the transmined sorders and inflammation. This can be also seen that the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1041 BP; 228 A; 295 C; 302 G; 216 T; 0 U; 0 Other;
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               GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCCCCCTGTTGTCCTG
                                                      GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
                                                                     GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG
                                                                                                           CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human microtubule motor protein #3"
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                             GGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTG
                                                 GGCAACAAGAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTG
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protein for treating cellular proliferation disorders by adding
candidate agent to a mixture of the target protein that
directly/indirectly produces ADP or phosphate.
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proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, modulators of the target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders and as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and angioplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention.
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Mismatches 0; Indels 0;
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fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, tastenosis, cardiach hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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                                                                                                       The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for
                             960
GGCAAAGTGGTAGATGGGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulators
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                                                                                                                                                                                                                                                                                                                                                                                                    cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertroph; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthrigarit rejection; inflammatory bowel disease; angioplasty.
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                             CTCACTCGCCTATTGCAGGACTCTCTGGGTGGC
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                                                                                                                                                                                                                                                                                                                                                          Human microtubule motor protein DNA #4.
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28-NOV-2000; 2000US-00724224.
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P-PSDB; ADQ60234.
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This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "KID protein"
/transl_except= (pos: 1. .5; aa: Met)
/note="Tris codon has an apparent 2 nucleotide insertion
that alters the reading frame"
                                                                                                                                                                                                                                                                                                                                         encoding the human kinesin-like DNA binding protein (KID) (SeqID 1)
                                                                                                                                                                                                                                                                                                                                                                    human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodilator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                           ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCGGG
      GGCAAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAAG
                                 CTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCACAGTATCCTTATTGCCAAC
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screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hyperrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, procedures including surgery and proliferation induced after medical procedures including surgery and angioplasty, This sequence represents DNA encoding a human microtubule
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Pred. No. 3.4e-295;
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therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length KID enzyme of the invention.
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                                                           Length 1115;
                                          Sequence 1115 BP; 241 A; 318 C; 333 G; 223 T; 0 U; 0 Other;
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                                                          Score 1038; DB 10;
Pred. No. 3.9e-295;
0; Mismatches 0;
                                                     99.7%; Scc.
100.0%; Pre
                                                                   Best Local Similarity 100.
Matches 1038; Conservative
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cardial encoding them. The invention also relates to a method of screening for Appase activity of microtubule stimulated Arpase activity, a method of testing for Appase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a macdilator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such a protein, and methods of treating cellular proliferation disorders such a cancer, hyperplasias, restences; cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restences; cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating autoimmune colliseasing induced after medical procedures including surgery and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule concordes the protein featured as SEQ ID NO:2, but this does not appear to be the case.
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978 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                            Disclosure, SEQ ID NO 1, 26pp; English
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2000US-00724224.
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28-NOV-2000;
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1038 GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1097
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    1538
    /*tag= a
    /produce = KID protein=
    /trans1 except= (pos: 4. .5; aa: Pro)
    /note= "This codon has an apparent 1 nucleotide deletion that alters the reading frame"

                                                                                                                                                                                                          DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 3)
                                                                                                                                                                                                                                     human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytoëtatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
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2000US-00597292
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20-JUN-2000;
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                                   Query Match 99.7%; Score 1038; DB 12; Best Local Similarity 100.0%; Pred. No. 3.9e-295; Matches 1038; Conservative 0; Mismatches 0;
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New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                   Human, microtubule motor protein, gene; ds; cellular proliferation disorder; cancer, hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angloplasty.
                                                                                                    DNA #2.
                                                                                                    Human microtubule motor protein
1114
                                             ВP
                                                                                                                                                                                                                                                   20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
                                            ADQ60229 standard; DNA; 1538
                                                                                                                                                                                                                                 06-MAR-2002; 2002US-00093317
1098 AAGGAGGTGATCAATCG
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                           (CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                               WPI; 2004-532491/51
                                                                                                                                                                                               US6762043-B1.
                                                                               23-SEP-2004
                                                                                                                                                                                                                  13-JUL-2004
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                                                                ADQ60229;
                                     ADQ60229
ID ADQ6
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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ArPase activity, a method of testing for ArPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or protein or act as a modulator of the binding characteristics or protein, and methods of treating callular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with Kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor protein useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating disorders associated with KID and for inhibiting KID and for treating disorders cassociated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and cassociated with KID and for inhibiting KID and for treating succimune and proliferation induced after medical procedures including surgery and and protein of the invention. Note: The specification states that this sequence encodes the protein featured as SEQ ID NO:4, but this does not appear to be the case.

Disclosure; SEQ ID NO 3; 26pp; English.

Score 1035.4; DB 12; Length 1538; Pred. No. 2.6e-294; 0; Mismatches 1; Indels 0; ( Sequence 1538 BP; 355 A; 432 C; 459 G; 292 T; 0 U; 0 Other; Query Match 99.5%; Best Local Similarity 99.9%; Matches 1036; Conservative

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ADQ09241 standard; cDNA; 2097 BP

ADQ09241

23-SEP-2004

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Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic
                                                                     thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis is cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
                                                                                                                                                                                                                                                                    Roussigne M, Clouaire T;
                                                    encoding cDNA SEQ ID NO:426
                                                                                                                                                                                                                                        (ENDO-) ENDOCUBE SAS.
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                             10-DEC-2002; 2002US-0432699P. 03-JUL-2003; 2003US-0485027P.
                                                                                                                                                                                           10-DEC-2003; 2003WO-IB006434
                                                                                                                                                                                                                                                                  Amalric F,
                                                                                                                                                                                                                                                                                      WPI; 2004-525034/50
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                                                                                                                                                       WO2004055050-A2.
                                                                                                                   human; gene; ss
                                                                                                                                     Homo sapiens
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                                                    Human KNSL4
                                                                                                                                                                                                                                                                   Girard J,
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Example 47; SEQ ID NO 426; 612pp; English.

The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of a gene. Also described: (1) a method of modulating the expression of a gene. Also described: (1) a method comprising the expression of a gene responsive a THAP responsive element in a pharmaccutical carrier; (3) a transcription factor decoy comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a transcription a THAP-family polypeptide or its biological fragment, or a nucleic acid and a method of constructing a cell which expresses a cell comprising a viral vector which comprise a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide; (8) a method of constructing a cell which expresses a comprising a THAP-family polypeptide; (9) methods of identifying a test compound that modulates transcription submothment or that modulates transcription at a THAP-family polypeptide; (9) methods of identifying a test compound that modulates transcription at a THAP-family polypeptide; (9) methods of identifying a test compound that modulates transcription at a THAP-family polypeptide; (10) methods of identifying a test compound that modulates transcription at a THAP-family polypeptide; (10) and condition selected from excessive or insufficient apoptosis, cardiovacular disease and neurodegenerative arising at chemokine or a THAP-family polypeptide in an individual; (11) a vector comprising a thap responsive promoter operably linked to a nucleic acid comprising a theorem about that a postibular and that expression or acivation mediated by a THAP-family polypeptide in an individual; c

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polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, oryostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the Sequence 2097 BP; 483 A; 592 C; 628 G; 394 T; 0 U; 0 Other; present invention. 

Gaps Query Match 99.5%; Score 1035.4; DB 12; Length 2097; Best Local Similarity 99.9%; Pred. No. 3e-294; Matches 1036; Conservative 0; Mismatches 1; Indels 0;

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183 279 GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGGGCAAGTGATCCCCCCTGT GTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACT GTGCGGGGCCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGCAGGAGACT 160 124

399 TATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGG 304

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1059 GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCCAACTTTGCTGCCAGGTCC 1023 963 AAAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTC 904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 1136 AAGGAGGTGATCAATTG 1040 1120 AAGGAGGTGATCAATCG 844 1060 1024 940 964 g 셤 ò 셤 8 g à 8

BP ADK40995 standard; DNA; 2099

ADK40995;

06-MAY-2004 (first entry)

Novel human kinase gene #15

cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase; himbibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; pain; adorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme; gene; ds. ADK40995

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Homo sapiens.

WO2003057841-A2.

31-DEC-2002; 2002WO-US041687

31-DEC-2001; 2001US-0343169P

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(GRIG/) GRIGORIEV I V. (SUDA/) SUDARSANAM S.

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WPI; 2003-587115/55.

603 669 663

New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders.

Claim 33; SEQ ID NO 102; 491pp; English.

723 819 783 843

784 AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGC

The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and encodes a naturally occurring kinase polypeptide; (d) encodes the polypeptide in (a), except that it lacks one or more, but not all, of an N-terminal domain, C-terminal catalytic domain, a catalytic domain, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-

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terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzhaimer's disease, of Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, infections caused by bacteria, infections caused by prions, infections caused by sexual dysfunction, mood disorders, attention disorders, cognition disorders, dysfunction, mood disorders, attention disorders, cognition disorders, dyskinselsa, metabolic disorders and organ transplant rejection. This sequence corresponds to the DNA encoding one of the
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Matches 1036; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders
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                       AACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCCCCCTGTTTGTCCTGGGC
                                                                                                                                                                     1061 GCCCCTGAGAGACGCTTCTACCTAGACACACTCCCCCACTCAACTTTGCTGCCAGGTCC
                                                                        AAAGTGGTAGATGCGCTGAATCAGGCCTCCTCGTGTACCTTATCGGGACAGCAGCTC
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784 AACAAGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate cancer antigen nucleotide sequence SEQ ID NO:288.
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diseases. AAF16506 to AAF16514 to
in the exemplification of the present
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                                                           Query Match

99.3%; Score 1034; DB 3; Length 2104;
Best Local Similarity 99.7%; Pred. No. 7.7e-294;
Matches 1034; Conservative 1; Mismatches 2; Indels 0,
                                       Sequence 2104 BP; 517 A; 580 C; 597 G; 400 T; 0 U; 10 Other;
 s, wounds, and infectious represent sequences used
   disorders, wounds,
AABS7303 represent
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for chaptorsisty, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations cresponsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was contained in electronic format directly from USPFO at
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1023
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GCCCCTGAGAGGCCTTCTACCTAGACACAGTCTCCGCACTTCAACTTTGCTGCCAGGTCC
                    1027 GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC
                                                                                                                                                                                                                                                                                                                 expressed sequence tag;
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25.5%; Score 265; DB 9; Length 464;
Best Local Similarity 77.6%; Pred. No. 1.7e-67;
Matches 333; Conservative 0; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                   Human; ss; sequencing by hybridisation; SBH; e.
genome mapping; biodiversity; genetic disorder
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                                                                     1024 AAGGAGGTGATCAATTG 1040
                                                                                      1087 AAGGAGGTGATCAATCG 1103
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STACHE-CRAIN E
DICKSON M C.
JONES L W.
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                                                                                                                                                                                   ACH44493 standard;
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(STAC/) (DICK/) 1
(JONE/) 1
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cc expression, comprising any of the 27,400 fully defined mucleotide expression, comprising any of the 27,400 fully defined mucleotide or engeneers or the specification. The probe is a single exon probe that concoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that concoding at least 8 amino acids of any of the 6888 amino acid molecule expression (comprising a plurality of single exon mucleic acid molecule cypression (comprising a plurality of single exon mucleic acid molecule comprising them of the datessable set of single exon mucleic acid probes is esparately can daddressable so amplifiable from the plurality), a single cycon microarray for measuring human gene expression, a vector comprising at least 8 contiquous amino acids of any of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of can of the above- mentioned amino acid of sequences (optionally with conservative amino acid acid soft and of the above- mentioned amino acid can easure gene expression, a method of providing methods of selling and/or licenaing single exon probes or microarrays to methods of selling and/or licenaing single exon probes or method of can record including data on the expression of a single exon probe cited above. The probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon probe of the invention. Note: The sequence data for this a human considered by the probes of the sequence of expensed or a si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804 AGAGAGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAA 863
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Local Similarity 98.7%;
es 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid probe for measuring human gene
                                                         CAAATACCAGTTTGATGCCTTCTATGGGGAGGAGTACTCAGCAGGACATCTATGCAGG
                                                                                                                                                                                                       Trancardadescaracterecraterretrestantandescanderescra
                                                                                                                                                                                                                                                                      217 CGGIGCCTGAGGAGCTGGCATTAC-ATCTCGATGCTTGGCAGCCCAGAGCAACCTGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCTGGACCCTGCTTCGGAGACCTTGGAATCCGAGAAGACTGCCGGGGGAATATCCT
                                                                                                                                                                    TTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTA
                                                                                                                                                                                                                                           TGGACCCACAGAGCTGGGAAGACGCACACAATGCTGGGCAGCCCAGAGCAACCTGGGGT
                                                                                                                                                                                                                                                                                                                      GATCCCGCGCGCCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAGGGTGCCGAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome derived single exon probe #10603.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-concession comprising a plurality of single exon nucleic acid molecule probes cited above, where each of the plurality of single exon nucleic acid probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wector comprising at least 8 contiguous amino acids of any of the above mentioned amino acid of probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above mentioned amino acid sequences (optionally with conservative amino acid substitutions), and solated antibody that binds specifically to a peptide cited above, methods of sequences (optionally with conservative amino acid substitutions) and conservations at customer desiring at omeasure gene expression, a method of providing a customer desiring and/or licensing single exon probes or microarrays to the above. The probe, methods mad apparatus are useful in gene capression analysis. The probes may be used as tools for surveying the above. The probes may be used as tools for surveying the above. The probes may be used as tools for surveying the above. The probes are used in identifying and characterising and encounter in determined in dentifying and characterising and encounter in determined in dentifying and characterising and encounted in definition, the probes are useful in dentifying and encounted in definition and encounted in definition and encounted in addition and encounte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 GTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCAGGAAAACTCTACCTGATT 747
                                                                                                                                                                                                                                                                                                                                                                                                  New human genome-derived single exon nucleic acid probes useful for huma gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGGAAAACTCTACCTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segdata.uspto.gov/sequence.html?DocID=20030194704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 24303; 80pp; English.
                                                                                                                                                                                                                                                                                                       Hanzel DK;
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                                                                                               03-APR-2002; 2002US-00029386.
                                                                                                                                               03-APR-2002; 2002US-00029386.
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Best Local Similarity
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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  US2003194704-A1.
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 TACCTGTTCGACGTGGCCTTTGACCGCCACCCAGGGGGGGTGGTGTATCAGGCCACC 345
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867
                          AGTGGAGCCATCAACACCTCCTGTTTGTCCTGGGCAAAGTGGTAGATGCGCTGAATCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention May have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectide or as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 TACCAGITIGAIGCCTICIAIGGGGAGGAGGAGTACTCAGCAGGACAICTAIGCAGGTICA
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                                                                                                                                                                                                                                                                                                                        gene; human; gene therapy; diagnostic marker; pharmaceutical.
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                                                                GGCCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGG
                                                                                  GCCCCCCCCCCTCGTATCGGGACAGCAGCACCACTCGCCTATTGCAGG
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Pred. No. 1.6e-43;
0; Mismatches 379;
                                                                                                                                                                                                                                                                                           Human cDNA of the invention SEQ ID NO:249
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                                                                                                                                                                                          ADM01564 standard; cDNA; 2095
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Yoshikawa T,
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Best Local Similarity
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997 AAGCTCACCCGGCTCCTGAAGGACTCTCGGGAAACAGCCGCACAGGGATGATCGCT 1056
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CCCACAGGCTGTGGGAAAACCTACACCATGCTGGGCACCAGGACCAGGAGCCTGGCATCTAT 465
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                                  430 IGGGCCCTITCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAAGGTATTAGACCTC
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2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1111 1111 1111 1111 1111 1111 1111 1
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; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Human
US-10-797-893-7
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US-10-797-893-7
Sequence 7, Application US/10797893
Spublication No. US20040142397A1
GENERAL INFORMATION:
J. APPLICANT: Beraud, Christophe
TITLE OF INVENTION: their use
TITLE OF. INVENTION: their use
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT FILING DATE: 2004-03-09
FRICH APPLICATION NUMBER: US/09/724,224
FRICH FILING DATE: 2000-11-28
FRICH APPLICATION NUMBER: 09/597,292
FRICH APPLICATION NUMBER: 09/597,292
FRICH FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                   99.8%;
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Best Local Similarity 99.9
Matches 1039; Conservative
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; Publication No. US20040142397A1
; GENERAL INFORMATION:
    APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel mctor proteins and met);
    TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 3
; LENGTH: 1538
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99.5%; Score 1035.4;
Best Local Similarity 99.9%; Pred, No. 0;
Matches 1036; Conservative 0; Mismatches
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US-10-797-893-3
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US-10-797-893-3
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; Publication No. US20040142397A1
; CENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: US-04-03-09
; FILE REFERENCE: 1044
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS ITILE OF INVENTION: CANCER PILE REFERENCE: 529452000122
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| Sequence 288, Application US/09925300
| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PALO
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT PILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: 601-03-08
| PRIOR PILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SOFTWARE PATENTIN VOWER: 200
| SEQ ID NOS: 1890
| SEQ ID NO 288
| LENGTH: 2104
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
LOCATION: (44)
OTHER INPORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (497)
OTHER INPORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (1323)
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Best Local Similarity 99.7
Matches 1034; Conservative
                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-925-300-288
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                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                        Query Match 25.5%; Score 265; DB 10; Length 464; Best Local Similarity 77.6%; Pred. No. 1e-74; Matches 333; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1177, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
GENERAL PROCHMATION:
APPLICANT: Moratis, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

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PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/749,586

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2059

SEQ ID NO 1177

EMCGHI- 24291
                                                                                        ; LOCATION: (1) ... (464)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705
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| LOCATION: (1)...(24291)
| OTHER INFORMATION: n = A,T,C or
US-10-087-192-1177
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                                  FEATURE:
NAME/KEY: misc_feature
              ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTCAGAGGACAACCGGCGCACAGGCAACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCC
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US-09-318-995-31705

i Sequence 31705, Application US/09918995

i Publication No. US20030073623A1

i GENERAL INFORMATION:

i APPLICANT: Hyeeq, Inc.

ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

ITILE OF INVENTION: ROW VARIOUS CDNA LIBRARIES

i FILE REPEREENCE: 20411-756

i CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

i PRIOR FILING DATE: 2001-07-30

i NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

i SEQ ID NO 31705

i LENGTH: 464
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Pred. No. 2.3e-103;
0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1180
LENGTH: 24525
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.8%;
Matches 445; Conservative
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; ORGANISM: Homo sapiens
US-10-087-192-1180
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US-10-029-386-24303

Sequence 24303, Application US/10029386

Publication Vo. US20030194704A1

Sequence 24303, Application US/10029386

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

CURRENT FILING DATE: 2001-12-20

UNWHER OF SEQ ID NOS: 34288

SOFTMARE: Annomax Sequence Listing Engine vers. 1.1
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     CAAGGTGGACCAGCGGGAACGTTTGGCCCCCATTTCGCCAGCGAGAGAAACTCTACCT
                           CCAGGTGGACCAGGGGGAAAACGTTTTGGCCCCATTTCGCCAGGGGAAAACTCTACCT
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIT: 014807, EVALUE 5.00e-37
OTHER INFORMATION: EST HUMAN HIT: BE392882.1, EVALUE 1.00e-125
OTHER INFORMATION: NT HIT: 916453817, EVALUE 1.00e-125
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Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-108-260A-249
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LENGTH: 232
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Publication No. US20030194704A1

GENERAL INPORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Harzel, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

LENGTH: 531
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                                                                             2939 AGGTATTAGACCTCTTGGATCCTGCATCAGGAGACCTCGTGATCCGCGAAGACTGCCCAG 2998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO CHRI6.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: WT HIT: AB017334.1, EVALUB 0.000+00

OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUB 2.000-36

OTHER INFORMATION: EST_HUMAN HIT: BF975048.1, EVALUE 1.000-126
 Pred. No. 2.2e-73;
0; Mismatches 61; Indels
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73.8%;
Local Similarity 73.8
hes 385; Conservative
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US-10-029-386-10603
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APPLICANT: Seringer, Olling A.M.,
APPLICANT: Seringer, Bryan D.,
APPLICANT: Zerthusen, Bryan D.,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-4802
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR PILING DATE: 2001-11-30
PRIOR PLING DATE: 2002-02-03
PRIOR PLING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-03
PRIOR PLING DATE: 2002-08-04
PRIOR PLING DATE: 2002-08-04
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-14
PRIOR PLING DATE: 2002-08-14
PRIOR PLING DATE: 2002-08-17
PRIOR PLING DATE: 2002-08-17
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PRIOR PLING DATE: 2002-08-17
PRIOR PLING DATE: 2002-08-17
PRIOR PLING DATE: 2002-08-17
PRIOR PLING DATE: 2002-08-17
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/334,627
PRIOR APPLICATION NUMBER: 60/331,641
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SOFTWARE: CuraSeqList version 0.1
               1117 CGGCCAAGAACATTAAGACTAG 1139
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                                                                                                                                                                                                                                          Sequence 301, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
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Maryankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Millet, Isabelle,
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Spytek, Kimberley A.
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Pastelli, Luca,
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Ji, Weizhen,
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Shenoy, Suresh G.
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Gangolli, Esha A.
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Ort, Tatiana,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 184.6; DB 16; Length
Pred. No. 1.3e-48;
0; Mismatches 379; Indels
TITLE OF INVENTION: No. US20040005560Alel full length cDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 249
LENGTH: 2095
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Best Local Similarity 53.7%;
Matches 463; Conservative
                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-249
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                                                                                                                                                                                                                                                      Length 3374;
                                                                                                                                                                                                                                                   Score 155.8; DB 16; Length
Pred. No. 2.9e-39;
0; Mismatches 317; Indels
                                                                                                                                                                                                                                                15.0%;
ilarity 54.0%;
Conservative
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                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                        FEATURE:
NAME/KEY: CDS
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Best Local Simi:
Matches 394;
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US-10-287-226-301
SEQ ID NO 301
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OTHER INFORMATION: fragment
OTHER INFORMATION: Nuclectide sequence of HsKipJa fragment used
OTHER INFORMATION: ATPase assay (Figure 5).
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                                                                                                                       FOR THEIR
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APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Davies Katherine A.
1TILE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR FILE REPERBNCE: 020552-001410US
CURRENT FELLIGE DATE: 2001-06-15
PRIOR PAPLICATION NUMBER: US 09/594,655
PRIOR APPLICATION NUMBER: US 09/594,655
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
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ilarity 51.2%; Pred. No. 3.2e-33;
Conservative 0; Mismatches 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 437; Conserv
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Sequence 6, Application US/0983096
Patent No. US20020110883A1
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew

RESULT 14 US-09-883-096-6

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ATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCCACTCAACTTTGCTGCCAGG 1020
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   GGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAACAAG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAGCGCTGCGGGAGGGGCCAACATCAACGGCTCTCTGCTGCCGCTCATCAACGTC 991
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                                                                                                CGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCGCAGTCATGCTGTG
                                                                                                                                                               CTCCTGGTCAAGGTGGACCAGCGGAACGTTTGGCCCCATTTCGCCAG-----CGAGAG
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CTCAATGCCTTGGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGGGACAGCAAA 921
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CTHER INFORMATION: Description of Artificial Sequence: HsKip3a gene. US-09-883-096-1.
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GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Tu, wing
APPLICANT: Tu, wing
APPLICANT: Tu, wing
APPLICANT: Patel, Umesh A.
APPLICANT: Davies, Katherine A.
TITLE OF INVERTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE;
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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llarity 51.2%; Pred. No. 4.7e-33;
Conservative 0; Mismatches 389;
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Patent No. US20020110883A1
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Best Local Similarity
Matches 437; Conserv
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AJ249840 Kenopus I
BC070549 Kenopus I
AF267849 Kenopus I
AC101927 Mus muscu
AX247007 Sequence
AC023831 Homo sapi
AC009133 Homo sapi
AC002301 Homo sapi
AC002301 Homo sapi
AF013119 Mus muscu
AC04377 Rattus no
AC133764 Rattus no
AC123460 Rattus no
                                                                                                                                                                  AC122537 Mus muscu
AC122863 Mus muscu
AC114179 Ciona int
AX83125 Sequence
AX094619 Homo sapi
AL929469 Zebrafish
CR34587 Danio rer
BCO57614 Mus muscu
U34658 Morone saxa
AC092563 Hylobates
AC092563 Hylobates
AC092562 Papio ham
AB017335 Homo sapi
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Patent: US 6387644-A 3 14-MAY-2002;
Location/Qualifiers
1. .1538
/organism="unknown"
/mol_type="unassigned pNA"
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Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 Bast Meadow Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
This CDS clone is a part of a collection of human full length
Harvard Institute of Proteomics. Bach CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the pDNR-DDAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones. PRI 13-MAY-2003 Z (bases I to 1998)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission Eisenstein, S., aer, J., Lin, Y., Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1998)
Ralnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.
Phelan,M. and Parmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor TAGAGATTGAGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGA linear Homo sapiens kinesin-like 4 mRNA, complete cds. BT007259.1 GI:30583356 FLI CDNA. 1501 AGGCTGAGGAAAAGGAGAACCATTGTCCCACAATGTGA 1538 AGGCTGAGGAAAAGGAGAACCATTGTCCCACAATGTGA 1538

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codon and before HindIII site to maintain reading frame, distribution: http://bioinfo.clontech.com/orfclones. Location/Qualifiers
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/note="Mutations: 1997:Stop->Leu"
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collection"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches
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Homo sapiens mRNA for kinesin-like DNA binding protein, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1048 ATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCTA
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                GCCTTGGGACCTGTTAAGCTGTCTCAGAAGAATTGCTTGGTCCACCAGAGGCAAAGAA
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Tokai,N., Fulimoto-Nishiyama,A., Toyoshima,Y., Yonemura,S., Tsukita,S., Inoue,J. and Yamamota,T.
Kid, a novel kinesin-like DNA binding protein, is localized chromosomes and the mitotic spindle
EMBO J. 15 (3), 457-467 (1996)
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AB017430 2 GT:4519442
Kid; kinesin-like DNA binding protein; kinesin family.
Homo sapiens (human)
Homo sapiens
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1468 ATTGAGAGGCTTAAGACGAAGCAAAAAAGAACTGGAGGCCAAGATGTTGGCCCAGAAGGCT
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HGPPSQVEDLERVEGITGKQMESFLKANILGLLABGGRCGAS"
E 2 (bases 1 to 2097)
S Tokai-Nishizumi, N. and Edamasu, M.
Direct Submission
AL Submission
AL Submitted (03-SEP-1998) Noriko Tokai-Nishizumi, The University of Tokyo, The Institute of Medical Science, Department of Oncology;
4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan (E-mail:cokanedai, Minato-ku, Tokyo 108-8639, Japan (E-mail:cokanedai) Minato-ku, Tokyo 108-8639, Japan (B-mail:cokanedai) Minato-ku, Tokyo 108-8639, Japan Tax:03-5449-5413)
T D38751:Submitted (02-Nov-1994)
Sequence updated (22-Feb-1999).
Sequence updated (22-Feb-1999).
L: 2097
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2117)

2. Strausberg, R.L., Feingold, E.A., Grouse, D.H., Derge, J.G., Altachul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M.; Hong, L., Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Scheefer, C.F., Morent, F., Staplecon, M., Soares, M.M., Morent, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lul, X., Gibbs, R.A., Fahey, J., Helton, E., Sodergren, E.J., Lul, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Santluz, J. Myer, Bouffact, G.G., Blakesley, W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myer, Schein, J.E., Jones, S.J., and Marrai, M.A. Generation and initial analysis of more than 15,000 full-length buman and mouse cDNA sequences.
                             mRNA linear PRI 29-JUN-2004
22, mRNA (cDNA clone MGC:40049
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Horoks,S.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                  Homo sapiens kinesin family member IMAGE:5241557), complete cds.
                                                                                                                                                                        BC028155.1 GI:20380446
                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                 VERSION
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                                                          DEFINITION
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IYAGSVQPILRHLLEGQNASVLAYGPTGAGKTHTWLGSPEQPGVIPRALMDLLQLTRE
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ADFERHFLPASRNRTVGATRINQRSSRSHAVLLVKVDQRERLAPFRQREGKLYLIDLA
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GSAHSILIANIAPERRFYLDTVSALNPAARSKEVINRPFTNESLQPHALGPVKLSQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGPPEAKRARGPEEETIGSPEPMAAPASASQKLSPLQKLSSMDPAMLERLLSLDRLD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTMLR PLSHRTVTGAKPLKKAVVMPLOLI OEQAASPNAEIHILKNKGRRKRLESLDAL
EPEEKAEDCWELQISPELLAHGROKILDLLNEGSARDLRSLORIGPKKAOLIVGWREL
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                                      clone="MGC:40049 IMAGE:5241557"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                  note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                          /product="kinesin family
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Best Local Similarity 100.0
Matches 1530; Conservative
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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Baher, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Baher, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.N.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Scheir, J.B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: B Row: f Column: 1 This clone was sected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6453817. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autocystic.ca.

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Urenla Skalska,
Duane Smallus, Jeff Stock, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
2134 bp mRNA linear PRI 29-JUN-2004
kinesin family member 22, mRNA (cDNA clone MGC:1573
                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MA-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                         Homo sapiens kinesin family m
IMAGE:3535435), complete cds.
                                                                                                 BC004352.1 GI:13279307
                                                                                                                                                 Homo sapiens (human)
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     GGTGCCGAGGCCCGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAG 548
                                                                                                                                                                                                                                              GAGCGGCACTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAG
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                                                                                                                                                 CGGGGGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT
                                                                                                                                                                            CGGGGGAATATCCTGATTCCGGGTCTCTCCCCAGAAGCCCATCAGTAGCTTTGCTGATTTT
                                                                                                                                                                                                                                                                                                                                             CGCTCCTCCCCCCAGTCATGCTGTCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                            CGCTCCTCCCCCCAGTCATGCTGTCCTCGTCAAGGTGGACCAGCGGGAACGTTTGGCC
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/gone="KIF22"

/note="synonyms: KID, OBP, OBP-1, OBP-2, :

/db_xref="LocusID:3835"

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99.5%; Score 1530; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches
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/db_xref="MIM:603213"
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                     904 ACTGGCCTATTGGAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT
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larity 99.9%; Pred. No. 3.9e-279;
Conservative 0; Mismatches 1;
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Motor proteins and methods for their u Patent: US 6387644-A 1 14-MAY-2002;
Location/Qualifiers

1. 1115/Qualifiers
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Sequence 1 from patent US 6387644.
AR210052 GI:21512182
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Unclassified.
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1 (bases 1 to 1464)
Beraud, C.
Motor proteins and methods for their Patent: US 6387644.A 7 14 MAY-2002;
Location/Qualifiers
                                                                                                               Query Match 95.0%; Score 1461; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CE (bases 1 to 2086)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Altschul, S.F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

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Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

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Boutfard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Boutfard, G. S., Krzywinski, M. I., Skalska, U., Sanchutz, J., Myers, R. W.,

Generation and intital analysis of more than 15,000 full-length

human and mouse cDNA sequences

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21704181. Location/Qualifiers
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/tleaue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-FB2-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
us musculus kinesin family member 22, mRNA (cDNA clone MGC:6456
MAGE:2615715), complete cds.
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Contact: MGC help desk
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                              Mus musculus (house mouse)
Mus musculus
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/gene="Kif22'
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boukpallarkiyi, L., Boukhgalter, B., Brown, A., Camarata, J., Capapojano, A., Chang, J., Chazaro, B., Cooke, P., Deakellano, K., Dewar K., Olara, J. S., Collymore, A., Cooke, P., Deakellano, K., Dewar K., Diaz, J. S., Dodge, S., Faro, S., Gords, Govete, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Bardina, K., Deakellano, K., Dewar K., Diaz, J. S., Dodge, S., Faro, S., Gords, M., Horton, L., Hulme, M., 111ev, I., Johnson, R., Jones, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Mactan, P., Korner, Y., Merbeters, R., Milor, H., Morbue, C., Morch, C., Mordonald, P., Major, J., Marthews, C., Macdonald, P., Merby, R., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Peterson, K., Phunkhang, P., Pieterson, R., Milow, J., Marthews, C., Morch, C., Mordonald, P., Major, J., Marthews, C., Morch, C., Mordonald, P., Major, J., Marthews, C., Morch, C., Mordonald, P., Spencer, B., Stange-Thomann, N., Stolasovic, N., Sartoss, M., Subramanian, A., Tatavis, M., Tatgillo, J., Washilton, M., Wall, K., Vo, A., Wilson, B., Wi, X., Waman, D., Young, G., Severy, P., Spencer, B., Santos, M., Zammer, A., and Zody, M. 2atloun, J., Zambek, L., Zammer, A., and Zody, M. 2atloun, J., Zambek, L., Zammer, A., and Zody, M. 2atloun, J., Boukpains, D., Marthews, C., Machen, C., Bouguslavkiy, L., Boukhgalter, B., Abouellell, A., Allen, M., Barna, S., Bratch, J., Chang, J., Chang, J., Chang, J., Gardyna, S., Landers, J., Chang, J., Chang, J., Gardy, J., Bouche, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Machen, C., Maniol, M., Manian, S., Walle, R., Walle, R., Walle, C., Lander, R., Senber, C., Rober, C., Machen, C., Manielle, M.
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Birren, B., Nusbaum, C. and Lander, E.
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                                                                                                   DB 6; Length 1041;
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                                                                                           Query Match 67.3%; Score 1035.4; DB 6
Best Local Similarity 99.9%; Pred. No. 4.9e-259;
Matches 1036; Conservative 0; Mismatches 1;
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                              Insert size: 151000, agarose-fp
Insert size: 150741; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; agarose-fp
Quality coverage: 11.8 in Q20 bases; aum-of-contigs
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                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: 117745
Center clone name: 158 A 6
Center clone name: 158 A 6
Sequenciny vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150558 bases at least Q40
Consensus quality: 150654 bases at least Q20
Consensus quality: 150687 bases at least Q20
                                                                                                                                                                                                                                                                           of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1518 33517: contig of 33517 bp in length 1518 33617: gap of 100 bp 1618 42736: contig of 9119 bp in length 1618 42836: gap of 100 bp 1837 84394: contig of 41558 bp in length 1835 gap of 100 bp 1837 84194: contig of 66547 bp in length 1615. Location/Qualifiers
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Pred. No. 1.1e-219;
0; Mismatches 288; Indels
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inote="assembly_fragment"
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Best Local Similarity 78.2%;
Matches 1136; Conservative
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Numerited (17-MAR.2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sirren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Canarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, P., Cooke, P., Corum, B., Colley, K., Dorats, L., Bayoslavkiy, L., Boukhgalter, B., Corum, B., Brickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoshan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, K., Liud, A., Mabbitt, R., Lindblad-Toh, K., Liu, K., Liud, A., Mabbitt, R., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McZarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McZarthy, M., Meldrim, J., Manjor, J., Manning, J., Malenga, V., O'Comnor, T., O'Donnell, P., Voleil, D., Oliver, J., Peterson, K., Seaman, S., Severy, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Tesfaye, S., Theodore, J., Topham, K., Traverse, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Voly, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Stamer, A., and Zody, M.
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramaeamy,U., Raymond,C., Retter,R., Rise,C., Rogov,P., Spencer,B., Schauer,S., Schupbac,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Teffaye,S., Theodore,J., Topham,K., Travers,M., Wassiliev,H., Voung,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (132-578-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 23, 2004 this sequence version replaced gi:45504330. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/rpt_fami
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 1, clone RP24-344C18
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                                                                                                                                                                                                                                                                                   1373 GGCCCCTCTGTTGAGTACCCCAAAGCGAGAGGGGATGGTGCTAATGAAGACAGTAGAAGA
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                                                          64530 ATCTCCAGCATCTGCTTCCCAGAA----
                   Mus musculus (house mouse)
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145840 CAGAATGCCAGTGTACTTGCCTATGGACCGACTGGGGCAGGAAGA--CACACAATGTTG 145783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145362 GAGGACACCGTCAGTCGCACAGGGCCATTCTGCTCAAGAGAGTGGAGTCCAT 145303
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                                                                                                                                                                                                                                                                                                                                                                     146137 GCGTCAGCCACCTCAGGACCGGGTCTTTGT---ATAAGCAAGGTAGGGATTGGCTGTCGT
                                                                                                                                                                                                                                                                                                                                                297 ACTCAGCAGGACATCTATGCAGGTTCAGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAGCCCAGAGCAACCTGGGGTGATCCGGGGGCTCTCATGGACCTCCTGCAGCTCAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145302 caacaccrccrcrrrgracresceaaagragresarscarraaaccaasscrccrccrca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145242 TATACCATACCAGGAGAGAGGCTCACTCGTTGCAAGACTCTCTGAGAGGCTCAC
                                                                                                                      GCGCCGCCGATCTCAGGAGCTGGTCGCTGTCGCTAAGCAAGATTGGAGCTACTCGTCGT
                                                                                                                                                                              177 GGAGCAAGTGATCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTAGAGATTGCTAAC
                                                                                                                                                                                                                                                                                              357 CAGAATGCCAGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGACGCACACAATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 AGGGAGGAGGGTGCCGAGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    657 GCTGATTTTGAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 ATCTACCAGGAGAAGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGA
                                                                                          28; Gaps
                                                          57.6%; Score 885.2; DB 10; Length 164759; llarity 78.2%; Pred. No. 1.1e-219; Conservative 0; Mismatches 288; Indels 28; G
/rpt_family="(TA)n"
37958..37986
/rpt_family="(GAA)n"
                                                            Query Match
Best Local Similarity
Matches 1136; Conserv
                     repeat_region
                                                                                                                                                                            117
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submission

Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 297639)

Bloom, T., Boquelavkiy, L., Boukhgalter, B., Caramta, J., Chang, J., Choepel, Y., Collymore, A., Cook, Cooke, P., Corum, B., Collymore, A., Cooke, P., Corum, B., Caramg, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Caramg, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Caramg, J., Caramg, J., Graham, L., Grand-Pierre, N., Hagos, B., Hall, J., Horton, L., Mulme, W., Iliev, I., Johnson, R., Johnson, R., Lindblad-Toh, K., Liu, J., Grand-Pierre, N., Machews, C., Macdonald, P., Manjor, J., Manning, J., Matchews, C., Macdonald, P., Major, J., Manning, J., Matchews, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasam, J., Schubback, R., Stedan, S., Severy, P., Somith, C., Spencer, B., Stange-Thomann, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Cophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Troopan, K., Travers, M., Wassiliev, H., Venkataraman, V.S., Viel, R., Voly, M., Voly, M., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zammer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 27, 2004 this sequence version replaced gi:31880232.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingron.edu/RM/RepeatWasker.html
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Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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241222: contig of 7622 bp in length
241322: gap of 100 bp
297639: 'contig of 56317 bp in length.
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/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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145182 TCATAGCATCCTCATTGTCAGCATTGCTCCTGAAAGATGTTTTTACCTGGAAACAATCTC 145123
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                                                                                                                                                                                                                                                                                                                                  AGAGGCAAAGAGACCCGAGGCCCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCATGGC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1253 AGCTCCAGCCTCTGCCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCAGCATGGACCC 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1313 GGCCATGCTGGAGCGCCTCCTCAGCTTGGACCGTCTGCTTGCCTCCCAGGGAGCCAGGG 1372
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 297639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144900 AGCCATGTTGGGAAAGCTCCTGAGTATGATGTTTGCTGGGTTCCAAGGGGAGCCAGAG
                                                                                            1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGAGAG
                                                                                                                                                                                                               145062 TGTACAACCTCAGGCCTTGACACCTGTTAAGCTGTCTCAGAAAGATCTGCTAAGGTTTATC
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HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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Mus musculus chromosome 1, clone RP24-275J1
Unpublished
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Sa Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavki, J., Cawkaller, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gardyna, S., Ferreira, P., Fitzhugh, W., Galagan, J., Garad-Pierre, N., Hagos, B., Hadford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kalls, C., Leworque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strawers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Leiter, M., Willer, M., McLander, A., Mand Zody, M., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., 
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23 Shases 1 to 196674)

84 Sharen, B., Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Beguslavkiy, L., Boukhgalter, E., Corum, B., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Dodge, S., Dooley, K., Dorris, L., Barickon, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Rerreira, P., FitzGerald, M., Gage, D., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamar, A., Karatas, A., Kalls, C., Landers, I., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Mannens, T., Micol, R., Mathews, C., Murphy, T., Macdonald, P., Mannens, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
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                                                                                                                                                                                          250 TCATAGCATCCTCATTGTCAGCATTGCTCCTGAAAGATGTTTTTACCTGGATACAATCTC 191
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus chromosome 1, clone RP23-202A19, complete sequence.
AC102127
                                                                                         1073 CGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGAGAG
                                                                                                                    190 AGCATTAAACTTCACTGCTAGGTCCAAGGAGGTGATTAACCAGGCTTTCACCAAAGGGAG
                                                                                                                                                                                                                                      130 TGTACAACCTCAGGCCTTGACACCTGTTAAGCTGTCTCAGAAAGATCTGCTAGGTTTAATC
                                                                                                                                                                                                                                                                                                                                                      agaggcaaagaaagccaaaaggcccrcaagaagaarcaacrgggagcccrgagrcraragc
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Mus musculus chromosome 1, clone RP23-202A19
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                                                                                                                                                                                                                                                                             GCGTCAGCCACCTCAGGACCGGGTCTTTGT---ATAAGCAAGGTAGGGATTGGCTGTCGT 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGAGGAGGGTGCCGAGGGCCGGCCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAG 536
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                                                                                                                                                                                                                        GCGGCGCCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGT
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                                                                                                               Length 297639;
                                                                                                                                                                    Indels
     /clone="RP24-275J1"
/clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                            48.4%; Score 744; DB 2; I 78.0%; Pred. No. 8.4e-183; ive 0; Mismatches 255;
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Matches 936;
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                 Submitted (10-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 196674)
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, I. Zimmer, A. and Zody, M.
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------ Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
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208. .1291
rpt_family="(CTA)n"
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/clone lib="RPCI-23 Female Mouse BAC"
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note="single clone coverage"
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complement (1974. .2067)
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3219. .3319
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family="L1_MM"
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omplement(13221. .13381)
rpt_family="B3A"
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omplement(15315. .15605)
rpt_family="RMER20"
omplement(16008. .16517)
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rpt family="(TG)n"
complement(16922. .17052)
rpt_family="B4"
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complement (9243. .9815)
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509: .4638
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516. .6570
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785. .4832
rpt_family="(CA)n"
626. .3688
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/note="clone bour
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tch 46.0%; Score 706.8; DB 10; Length 196674; al Similarity 73.3%; Pred. No. 4.2e-173; 10018; Conservative 0; Mismatches 357; Indels 12; Gaps	TGTGCGACTGCGGCCATTTGTGGATGGAACGGGGGGGGAGCAAGTGATCCCCCCTGTGTGCG 	GGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAACCACCAGGAGACTCTCAA 			AGTGCAGCCCATCCTAAGGCACTTGCTGGAAGGCCAGAATGCCAGTGTGCTTGCCTATGG	ACCCACAGAGACTGGGAAGACGCACAATGCTGGGCAGCCCAGAGCAACCTGGGGGGGGGG	TGATTE TO COCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCO		GGCCATGGGCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAGGAGAGATTTAG 	ACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCC	ıccı cıtatatat ceti ceat cadada ecta gitatat cada a titatatat cadada a catee	TGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGGGGCACTTCC	TGCCAGCCAGTCGAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCGCA	reccaeccretagaaarcaagtreragaagcractcrectraagcagterracata	GTCATGCTGTCCTGGTCAAGGTGGACCAGGGGGAACGTTTGGCCCCATTTCGCCCAGC	PAGAGGGAAAACTCTACCTGATTGACTTGGGTCAGAGGACAACGGCGCGCACAGGCA		ACAAGGGCCTTCGGCTAAAAGAGAGTGGAGCCATCAACACCTCCCTGTTTGTCCTGGGCAAAAAAAA	ACCAGIGCAIICAACICAAAAAAAGAGGCGCCAICAACCAGCIIGCII	ANGIGGIAGA COCCIONAL CANONICO DE LA MAGIGGAGGATACATATATACAGGACAGAAAAATCA	CICGCCTAITGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTAITGCCAACATTG	ITTGCCTATTGCCAGACTCTCTGGAAGGCTCAGCTCATAACATCATCATTACCAACACTG	CCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCCA 	AGGAGGTGATCAATCGGCCTTTACCAATGAGAGCTGCAGCCTCATGCCTTGGGACCTG		TTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAGAGCCCGAGGCCCTG
ry Ma t Loc ches	143 7	203 (	263	101752 /	323 7	383 /	439	101932	499 (	559	102052	619	619	102171	739	799	102290	859	n (	102408	979	102468	1039	9	102588	1159
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Search completed: November 10, 2004, 13:18:01 Job time : 6803.66 secs Adj95077 Novel NOV Aba94616 Nucleotid Abs7216 DNA encod Aai70088 Human kin Aal39519 DNA encod Adm81051 Human H8K Aby47991 Human pro

Abs57215 Human kin

Abt40796 Toxicity
Abd73061 Human kin
Aal56806 DNA encod
Adb66785 DNA encod
Abd73062 Human kin
Asi56807 DNA encod
Adb66787 DNA encod
Adb66787 DNA encod

Adq19012 Human sof Ab128591 Drosophil Ab116733 Drosophil Ab116732 Drosophil Adc30338 Human nov Adc30569 Human nov

Adc10189 Human NOV Aba94615 Human H8K

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Title: Perfect (

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Database :

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frans1 except= (pos: 4. .5; aa: Pro)
/note= "This codon has an apparent 1 nucleotide deletion
that alters the reading frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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20-JUN-2000; 2000US-00597292.
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                                          WPI; 2003-706919/67.
P-PSDB; ADC23340.
  Homo sapiens
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  Adc23339 DNA encod
Adg60229 Human mic
Adg60231 Human KNS
Adc40995 Novel hum
Adc2333 Human mic
Adf60233 Human mic
Adc2331 DNA encod
Adg60227 Human mic
Adc2331 DNA encod
Adg60227 Human mic
Adc7331 DNA encod
Adg60221 Human mic
Adc7331 Human mic
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Adc7331 Human mic
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Ach7108 Human gen
Ach7108 Human gen
Ach71108 Human gen
Ach71108 Human gen
Ach71108 Human mic
Adm01564 Human cDN
Ado4181 DNA encod
Ady35073 Novel NOV
Abx34596 Human mid
Abx34596 Human mid
                                                                                                                                                   9, 2004, 09:45:10 ; Search time 795.24 Seconds (without alignments) 10152.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                              1 atgcagccgcgggcggctcg.....accattgtcccacaatgtga 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                       5.1.6
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       4134886 segs, 2624710521 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                       GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum Match O%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           - nucleic search, using sw model
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                                                                              This invention relates to a novel method for high throughput screening systems used to identify compounds for the treatment of cellular proliferation disorders. Specifically, it refers to candidate agents that are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP to phosphate. Furthermore, this activity of an be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a method that identifies modulators of the target protein, which is a immunoundulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasis, thestendish, cardiac hypertrophy, immune disorders and inflammation. This polymucleotide sequence is human KID DNA (SeqID 3) encoding a full length KID enzyme of the invention.
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                                                                                                                                                                                                                                                                                                             The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for medulators of a motor protein which has microtubule stimulated Arpase activity, a methods of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target compose, and includance or the binding characteristics or compose, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating cellular proliferation disorders such as an inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of modors of the invention, inflammatory bowel disease and considered modors of the invention. Note: The specification states that this capen considered modors of the invention. Note: The specification states that this does not appear to be the case.
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                                                                                                                                                                                                                   New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
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20-JUN-2000; 2000US-00597292
28-NOV-2000; 2000US-00724224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thanatos-associated protein; THAP; THAP responsive gene; THAP family; THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
Modulating expression of a Thanatos (death)-Associated Protein (THAP)
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The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of of modulating the expression of a gene responsive to a THAP/fohemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a fragment; (7) a method of constructing a cell which expresses a succeeding with a condition mediated by a THAP/chemokine complex symptoms associated with a condition mediated by a THAP/chemokine complex

Example 47; SEQ ID NO 426; 612pp; English.

antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase; cancer; peripheral nervous system; central nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; neurological disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesis; metabolic disorder; organ transplant rejection; enzyme; gene; ds.

31-DEC-2002; 2002WO-US041687 31-DEC-2001; 2001US-0343169P

WO2003057841-A2. Homo sapiens.

17-JUL-2003

cytostatic; immunomodulator; cardiant; neuroprotective;

human kinase gene #15.

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New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and

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Grigoriev IV, Sudarsanam

WPI; 2003-587115/55.

(GRIG/) GRIGORIEV I V. (SUDA/) SUDARSANAM S.

The invention elates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a), (c) hybridizes under stringent conditions to (a) and conditions to (a) and conditions to (b) the control of an encodes a naturally occurring kinase polypeptide; (d) encodes the collegation of (a), except that it lacks one or more, but not all, of an condition of terminal domain, a coiled-coil structure region, a spacer region and a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzhaimer's disease, pain, viral infections, infections caused by fund; ocular diseases, methods infections caused by fund; ocular diseases, methods of secretal, infections caused by fund; ocular diseases, methods of disorders, dyskinesias, metabolic disorders, cognition disorders, dyskinesias, metabolic disorders and organ transplant control of the control of t 125 148 65 88 ATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCTCCA accececececrearce de a de consecuencia de consecuente de consecuencia de conse ATCTCAGGGGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCGTCCTCCA GCCGCGCGCCGCTCCACGCAGCCAGCGACGCGAGATGGCGGCAGCTTCAGCGGCGGCG Gaps ä DB 10; Length 2099; Sequence 2099 BP; 484 A; 592 C; 628 G; 395 T; 0 U; 0 Other; Indels ö 98.8%; Score 1519; D; 99.9%; Pred. No. 0; ive 0; Mismatches 33; SEQ ID NO 102; 491pp; English, kinase polypeptides of the invention Query Match
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ADK40995 standard; DNA; 2099

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 7)
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are capable of modulating the activity of target proteins having motor domains, such that the target protein directly or indirectly produces ADP or phosphate. Furthermore, this activity can be determined using fluorescence or absorbance readouts. The present invention describes a method that identifies modulators of the target protein, which is a farmesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, testenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleoride sequence is human KID DNA (SeqID 7) encoding a full length KID enzyme of the invention.
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1024 AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCGACCT
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요 Š 유 ò 셤

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The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders as adinfilammation, for treating disorders as associated with kinesin-like DNA conding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor protein seful for treating cellular consistence of motor infilammation, for treating autoimmune disorders and inflammation, for treating autoimmune consistence of seases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angloplasty. This sequence represents DNA encoding a human microtubule consistence of the invention.
                                                                                                                                                                                                                                                                             New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 7; 26pp; English.
                                        20-APR-1999; 99US-00295612.
20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
06-MAR-2002; 2002US-00093317
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P-PSDB; ADQ60234.
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ö Query Match

95.0%; Score 1461; DB 12; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 0; Indels 0; Sequence 1464 BP; 342 A; 409 C; 428 G; 285 T; 0 U; 0 Other;

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                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.
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method that identifies modulators of the target protein, which is a kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants, immunomodulators and antiinflammatories. Accordingly, through gene therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 1) encoding a full length KID enzyme of the invention.
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Pred. No. 6.5e-296;
0; Mismatches 1; Indels
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Best Local Similarity 99.9%;
Matches 1113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA binding protein (KID) (SeqID 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                      CCINCAGCITIGGACCGICTGCCTGCCTCCCAGGGGAGCCAKGGGGCCCCTCTGTTGAGTA
                                                                                                                                                                                                                                      CCCCAAAGCGAGAGGGGATGGTGTAATGAAGACAGTAGAAGAGAAGGACCTAGAGATTG
                                                                                                                                                                                                              AGAGGCTTAAGACGAAGCAAAAAGAACTGGAGGCCAAGATGTTGGCCCCAGAAGGCTGAGG
                                                                                                                      CCCCAAAGCGAGGCGGATGGTGCTAATGAAGACAGTAGAAGAAGGACCTAGAGATTG
                            CCT-CAGCTTGGACCGTCTGCTTGCCTCCCAGGGGAGCCAGGGGGCCCCTCTGTTGAGTA
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                                                                                                                                                                                                                                                                                                      AAAAGGAGAACCATTGTCCCACAATG 1535
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associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule motor protein of the invention. Note: The specification states that this sequence encodes the protein featured as SEQ ID NO:2, but this does not
                                                                                                                                                                                                                                                                                                                                                                                  CGGCGATCTCAGGAGCTGGTCGCTGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC
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                                                                                                                                                                 12; Length 1115;
                                                                                                                                                                                                                                0 Other;
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                                                                                                                               C; 333 G; 223 T; 0 U;
                                                                                                                                                               Score 1112.4; DB 1;
Pred. No. 6.5e-296;
0; Mismatches 1;
                                                                                                                                Sequence 1115 BP; 241 A; 318
                                                                                                                                                               72.3%;
                                                                                                                                                                                              Matches 1113; Conservative
                                                                                                 appear to be the case.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for andulators of a motor protein which has microtubule stimulated ATPasse activity, a method of testing for ATPasse activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders
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                                                                                                                                           ATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                                                                     961 ATCGGGACAGCACACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; microtubule motor protein; gene; ds; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
               1114
                                                                                                                                                                                                                           ACTITIGCTGCCAGGTCCAAGGAGGTGATCAATTG 1114
                                                                                                                                                                                                            ACTITIGCTGCCAGGTCCAAGGAGGTGATCAATCG
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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ACTCGCCTATTCCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 1037
therapy, they can be used for the treatment of cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. This polynucleotide sequence is human KID DNA (SeqID 5) encoding a full length KID enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCATTTCGCCAG
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                                                                                                                                                                                                                                                                                                                                                 GGTTCAGTGCCAGCCCATCCTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCC
                                                                                         Score 1035.4; DB 10; Length 1041; Pred. No. 1.1e-274; 0; Mismatches 1; Indels 0;
                                                                228 A; 295 C; 302 G; 216 T; 0 U; 0 Other;
                                                                                          Query Match 67.3%;
Best Local Similarity 99.9%;
Matches 1036; Conservative C
                                                                    Sequence 1041 BP;
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                                                                                                                                                                                                                                                                                                                                         DNA encoding the human kinesin-like DNA binding protein (KID) (SeqID 5).
                                                                                                                                                                                                                                                                                                                                                                human; gene; ds; motor domain; kinesin-like DNA binding protein; KID; cytostatic; cardiant; immunomodulator; antiinflammatory; gene therapy; cancer; hyperplasia; restenosis; cellular proliferation disorder; cardiac hypertrophy; immune disorder; inflammation.
                                                                                    ATCGGGACACCAGCTCCCCTATTGCAGGACTCTCTGGGGTGGCTCAGCCCACAGTA
                                                                                                                         TCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCA
                      Identifying a candidate agent as modulator of function of a target protein for treating cellular proliferation disorders by adding a candidate agent to a mixture of the target protein that directly/indirectly produces ADP or phosphate.
                                                                                                                                                                            ACTITGCTGCCAGGTCCAAGGAGGTGATCAATCG 1114
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GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGAGCAAGTGATCCCCCCTGT 123
   diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents DNA encoding a human microtubule
                                                                                                                                                                                                            GGTCGCTGTCGCCTAAGCAAGATTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG
                                                                                                                                                                                                                                                              GTGGCTGTGCGACTGCGGCCATTTGTGGATGGAACAGCGGGAGCAAGTGATCCCCCTGT
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                                                                                      Sequence 1041 BP; 228 A; 295 C; 302 G; 216 T; 0 U; 0 Other;
                                                                                                                      Score 1035.4; DB 12;
Pred. No. 1.1e-274;
); Mismatches 1; I
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                                                        motor protein of the invention.
                                                                                                                      Query Match 67.3%;
Best Local Similarity 99.9%;
Matches 1036; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening cor medulators of a motor protein which has microtubule stimulated Arpase activity, a method of testing for Arpase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a madulator of the binding characteristics or protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune disorders as such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating autoimmune
                                                                      1023
904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
                                 cellular proliferation disorder, cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human microtubule motor protein #3"
                                                                                                                                                                                                                                                                                                                                                           Human; microtubule motor protein; gene; ds;
                                                                                                                                                                                                                                                                                                                            microtubule motor protein DNA #3
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                                                                                                                      AAGGAGGTGATCAATTG 1040
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20-JUN-2000; 2000US-00597292.
28-NOV-2000; 2000US-00724224.
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                                                                                                    AAGGAGGTGATCAATCG
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or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the coll transformed or transfected with an expression vector of; an isolated or mithody, or its antispen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient; a fusion protein comprising at least the polypeptide; an optimized that hybridises to the polymucleotide under moderately catingent conditions; a method for stimulating and/or expanding T cells specific for a tumour protein; an isolated T cell population comprising T component consisting of carriers and immunostimulants, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a second component selected from the polymucleotides, proteins, and a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide of, or an antibody and a comportion reagont consisting of a reporter group. The polympetide, and consisting of a reporter group. The polympetide, and consisting of a reporter group. The polympetides and consisting of a reporter group. The polympetides and consisting of a reporter group. The polympetides and consisting of a reporter group. The polympetides and consisting of a reporter group. The polympetides and consisting of a reporter group. The polympetides and consisting of a reporter group or proteins.
                                                         GCCCCTGAGAGACGCTTCTACCTAGACACAGTCTCCGCACTCAACTTTGCTGCCAGGTCC 1097
904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCACAGTATCCTTATTGCCAACATT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent consisting of a reporter group. The polypeptides and polymucleotides are useful as vaccines for the treatment or prevention of lung cancer, and for diagnosis and monitoring of such cancer. The polymucleotide, polypeptide and antigen presenting cells can be used to simulate or expand T cells specific for a tumorous protein. The polymucleotides may be used as probes or primers for nucleic acid hybridisation, and in the preparation of ribozyme molecules for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumor lung proteins and nucleic acids encoding the proteins, useful as vaccines and for treating, preventing, diagnosing or monitoring lung
                                                                                                                                                                                                                                                                                                                                                                                                   Human; 88; gene; lung cancer; cytostatic; tumour; vaccine.
                                                                                                                                                                                                                                                                                                                                                               Human lung cancer associated cDNA SEQ ID 131
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                                                                                                                                      AAGGAGGTGATCAATTG 1040
                                                                                                                                                                                                                                                 ABK70260 standard; cDNA; 491 BP.
                                                                                                                1098 AAGGAGGTGATCAATCG 1114
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10-OCT-2000; 2000US-0239440P.
29-JUN-2001; 2001US-0301928P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
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                                                                                                                                                                                                                                                                                                                                          1070 CTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTTACCAATGA
                                                                                                                                                                                                                                                                                                                                                                     61 CTCCGCACTCAACTTTGCTGCCAGGTCCAAGGAGGTGATCAATCGGCCTTTT-CCAATGA
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                                                                                                                                                                                                                                           1010 AGCCCACAGTATCCTTATTGCCAACATTGCCCCTGAGAGACGCTTCTACCTAGACACAGT
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inhibiting expression of tumour polypeptides and proteins in tumour cells. The present sequence is one of the 183 lung cancer associated polynucleotides
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudduth-Klinger J;
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                                                                                                                                            Length 491;
                                                                                               C; 136 G; 88 T; 0 U; 0 Other;
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                                                                                                                                         Score 480; DB 6; L
Pred. No. 9.3e-122;
0; Mismatches 0;
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                                                                                               Sequence 491 BP; 127 A; 140
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                                                                                                                                                                                           Matches 491; Conservative
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                                                                                                                                                             Local Similarity
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                                                                                                                                              Query Match
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cDNA libraries, useful

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Jones

Dickson MC,

Stache-Crain B,

Drmanac RT, Labat I,

WPI; 2003-615964/58

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LABAT I. STACHE-CRAIN DRMANAC R T.

LABA/)

DICKSON M C. JONES L W.

(STAC/) (DICK/)

30-JUL-2001; 2001US-00918995. 30-JUL-2001; 2001US-00918995

17-APR-2003

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                                                                                                                 The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding
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genome mapping; biodiversity; genetic disorder.
                                                            New polynuclectides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer.
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    Lamson
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             Drmanac S, Labat I; WL, Stache-Crain B;
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    Kassam A,
                                                                                                                                                                                                                                                                         Indels
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   Pot D,
                      Jones WL,
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  Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
D, Kita D, Garcia V, Jone
                                                                                               Claim 1; Page 1080; 1193pp; English
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nilarity 98.4%;
Conservative 0
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                                           WPI; 2001-530177/58
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Best Local Similarity
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Reinhard C,
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 CAAATACCAGTTTGATGCCTTCTATGGGGAGGAGGAGTACTCAGCAGGACATCTATGCAGG 319
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New polynucleotide sequences obtained from various cDNA libraries, t as hybridization probes, as oligomers for PCR, for chromosome and genapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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Pred. No. 1.7e-62;
0; Mismatches 95
                                                                                                                                                                                                          Claim 1; SEQ ID NO 31705; 44pp; English.
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smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

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DB 12; Length 531;

Sequence 531 BP; 117 A; 153 C; 149 G; 112 T; 0 U; 0 Other;

Query Match

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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
396 CCTCCTGGACCCTGCTTCGGGAGACCTTGGAATCCGAGAAGACTGCCGGGGGGAATATCCT 455
                                                                                                                                              Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                            Human genome derived single exon probe #10603.
                                                                                                                                                                                                                                                                                                                                                                        Claim 15; SEQ ID NO 10603; 80pp; English.
                                                                           ACH77408 standard; DNA; 531 BP.
                                                                                                                                                                                                                                                                                            Penn SG, Rank DR, Hanzel DK
                                                                                                                                                                                                                          03-APR-2002; 2002US-00029386
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                                                                                                            (first entry)
                 GATTCCGGG 628
                                  GATTCCGGG 464
                                                                                                                                                                                                                                                          (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                                                                                                                        US2003194704-A1
                                                                                                                                                                        Homo sapiens
                                                                                                             29-JUL-2004
                                                                                                                                                                                                         16-OCT-2003.
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined a sequences in the specification, or their complements or fragments, and encoding at least 8 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-captressed in human cells or tissues. Also included are a spatially-captressed in human cells or amplifiable from the plurality, a single exon addressably isolatable or amplifiable from the plurality), a single compression (comprising a plurality of single exon mucleic acid above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wethod of contiguous amino acids of any of the above-mentioned amino acid of contiguous amino acids of any of the above-mentioned amino acid of selling and/or licensing single exon probes or microarrays to methods of selling and/or licensing single exon probes or microarrays to containe which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying contisues to detect the presence of expression of a single exon microarrays. The probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising single exon microarrays.

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817
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                                                                                                                                                                                                                   94 GATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGCAAGAGGCCTTCGGCTAAA 153
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                                            Indels
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Score 233.2; DB
Pred. No. 1e-53;
0; Mismatches
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  15.2%;
ilarity 98.7%;
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Matches 235; Conserv
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US-09-724-224-3
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US-10-093-317-3
; Sequence 3, Application US/10093317
; Sequence 3, Application US/10093317
; General No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR PILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                 1501 AGGCTGAGGAAAAGGAGAACCATTGTCCCACAATGTGA
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k; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.0%;
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APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: Human kinesins
FILE REFERENCE: CYCOPO36
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                              TYPE: DNA
ORGANISM: Human
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Sequence 34, Application US/09595684B
Patent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: Vaisberg, Eugeni

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                                                                                                GAGGAAGAGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTGCCTCCCAGAAA
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AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGACCT
              1024 AAGGAGGTGATCAATCGGCCTTTTACCAATGAGAGCCTGCAGCCTCATGCCTTGGGACCT
                                                  GTTAAGCTGTCTCAGAAAGAATTGCTTCGTCCACCAGAGCCAAAGAGAGCCCGAGGCCCCT
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; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT PILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; RIOR APPLICATION NUMBER: 09/724,224
; RIOR APPLICATION NUMBER: 09/724,224
; ROOFTWARE: PRESENCE FOR WINDOWS 8
; SOFTWARE: PRESENCE FOR WINDOWS VERSION 4.0
; SEQ ID NO 7
; LENGTH: 1464
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95.0%; Score 1461; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-10-093-317-7
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                 ATTTTGAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCA
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Sequence 1. Application US/10093317

GENERAL INFORMATION:
THE OF INVENTION: Christophe
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
TITLE OF INVENTION their use
TITLE TELENT FILING DATE: 2002-03-06
PRIOR PRICE TING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FasteEQ for Windows Version 4.0
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US-09-724-224-1

1 Sequence 1, Application US/09724224

2 Sequence 1, Application US/09724224

3 GENERAL INFORMATION:

4 APPLICANT Beraud Christophe

7 TILE OF INVENTION: their use

7 TILE OF INVENTION: their use

7 TILE OF INVENTION: their use

7 CURRENT APPLICATION NUMBER: US/09/724,224

7 CURRENT FILING DATE: 2000-11-28

7 FILE REFERENCE: 1044

7 CURRENT FILING DATE: 2000-16-06

7 FILOR PILING DATE: 2000-06-0

8 FILOR FILING DATE: 2000-06-0

9 SOFTWARE: FastSEQ for Windows Version 4.0

1 SEQ ID NO 1

1 LENGTH: 1115
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Pred. No. 3.1e-309;
0; Mismatches 1;
                                                                                                                AACCATTGTCCCACAATGTGA 1538
                                                                                                                                72.3%;
99.9%;
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Best Local Similarity 99.9
Matches 1113; Conservative
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; ORGANISM: Human
US-09-724-224-1
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; TYPE: DNA
; ORGANISM: Human
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                                                                        AGCAGGACATCTATGCAGGTTCAGTGCCCATCCTAAGGCACTTGCTGGAAGGGCAGA
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                                            CAAGTGATCCCCCCTGTGTGCGGGGCATGGACAGCTGCTCTCTAGAGATTGCTAACTGGA
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RESULT 8 US-09-724-224-5

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; Patent No. 6387644
; GENERAL INFORMATION
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; TITLE OF INVENTION: their use
; TILE REFRIENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT APPLICATION NUMBER: 09/597,292
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENTH: 1041 Length 1041; ö for 1; Indels Query Match 67.3%; Score 1035.4; DB 3; Best Local Similarity 99.9%; Pred. No. 3.8e-287; Matches 1036; Conservative 0; Mismatches 1; I 798 8

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	Qy         798 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC         857           Db         724 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGTCAGAGGACAACCGGCGCACAGGC         783           Qy         858 AACAAGGGCCTTCGGCTAAAAGAGACCATCAACACCTCCCTGTTTGTCCTGGGC         917           Db         784 AACAAGGGCCTTCGGCTAAAAGAGAGCCATCAACACCTCCCTGTTTTGTCCTGGGC         843           Qy         918 AAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTTTGTCCTGGGC         917           Db         944 AAGTGGTAGATGCGCTGAATCAGGGCCTCCCTCGTGTTATCGGGACAGCTC         903           Qy         978 ACTCGCCTATTGCAGACTCTCTGGGTGGCTCAGTACCTTATTGCCAACATT         1037           Db         904 ACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCTCATTTTTGCCAACATT         963           Qy         1038 GCCCCTGAGAGACTCTCTAGGTGGCTCAGCCCACAGTATTTTTGCTACACATT         963           Qy         1038 GCCCCTGAGACACTCTCTAGGTGGCTCCACACATTTTGCTGCCAGGTC         1037           Db         964 GCCCCTGAGACACTCTACACACTCCCGCACCACACATTTGCTGCCAGGTCC         1037           Qy         1038 AAGGAGGTGATCAACACTCTCCCGCACCACACACACACTTGCTGCCCACACACTTTGCTGCCACACACTTTGCTGCCACACACTTTGCTGCCACACACTTTGCTGCCACACACTTTGCTGCCACACACA	RESULT 10 US-09-883-096-1 is 36-90-883-096-1 is 36-90-883-096-1 is 36-90-883-096-1 is 36-90-883-096-1 is 36-90-883-096-1 is 40-90-883-096-1 is 40-90-883-096-1 is 40-90-883-096-1 is 40-90-90-90-90-90-90-90-90-90-90-90-90-90
Db   724   CGAGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC	RESULT 9 US-10-093-317-5 Sequence 5, Application US/10093317 Sequence 5, Application US/10093317 Sequence 5, Application US/10093317 Sequence 5, Application US/10093317 TITLE OF INVENTION: TITLE OF INVENTIO	QY         78 GGTCGCTGTCGGCTAAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG 137           Db         4 GGTCGTTCGGCTAAGCAAGTTGGAGCTACTCGTCGTCCACCTCCAGCTCGCGTAAGG 63           Oy         138 GTGGCTGTCGCTTAGCAGCTACTCGTCGTCCACCTCCAGCTAAGG 63           Oy         138 GTGGCTGTCGCACTTGTGGAACAGCGGAAGCTGATCCCCCTGT 123           Oy         198 GTGCGGGCATTGCACTTCTTGTGGATTGCTAACTGGAGCAACTCCCCCTGT 123           Oy         124 GTGCGGGCATTGATGCTCTTCTATGGGAACTGCAGGAACCACCAGGAGACT 183           Oy         258 CTCAAATACCAGTTTGATGCTCTCTATGGGAACTCTCAGCAGGAACTCTATGCA 317           Db         184 CTCAAATACCAGTTTGATGCTTCTATGGGAAGGAGTACTCAGCAGGAACTCTATGCA 243           Oy         258 CTCAAATACCAGTTTGATGCTTCTATGGGAAGAGGAGTACTCAGCAGGACATCTATGCA 243           Oy         244 GGTTCAGTGCACCTTCTATGGGAAGAGCAGAATGCCAGTGCTTGCT

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APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Craven, Andrew
APPLICANT: Dates, Wings
APPLICANT: Partel, Umesh A.
TITLE OF INVENTION: NOVEL MOTTOR PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 6
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ORGANISM: Artificial Sequence
SENERAL INFORMATION:
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OTHER INFORMATION: protein gene HeKip3a (Figure 1).
OTHER INFORMATION: Description of Artificial Sequence: HeKip3a gene.
                                                                                                                                                27;
                                                                                                 DB 4; Length 4108;
                                                                                              Query Match 9.0%; Score 138.6; DB 4; Length Best Local Similarity 51.0%; Pred. No. 1.8e-29; Matches 448; Conservative 0; Mismatches 404; Indels
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: HsKip3a OTHER INFORMATION: fragment OTHER INFORMATION: Nucleotide sequence of HsKip3a fragment used OTHER INFORMATION: ATPase assay (Figure 5).
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Pred. No. 3.5e-29;
0; Mismatches 389;
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8.9%;

Best Local Similarity 51.2%;

Matches 437; Conservative 0
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RESULT 11 US-05-8813-096-6 'Sequence 6, Application US/09883096 'Parent No. 6680369

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                  GCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCCGCAGTCAT 743
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| Patent No. 6368841
| GENERAL INFORMATION |
| APPLICANT: Beraud, Christophe |
| APPLICANT: Breadman, Richard |
| TITLE OF INVENTION: their use |
| FILE REFERENCE: 1045 |
| CURRENT APPLICATION NUMBER: US/09/724,508 |
| CURRENT FILING DATE: 2000-11-27 |
| PRIOR PILING DATE: 2000-07-21 |
| NUMBER OF SEQ ID NOS: 2 |
| SOUTHARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO |
| LENGTH: 897
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Pred. No. 5.4e-27;
0; Mismatches 356; Indels 72
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; ORGANISM: Human
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: (472)...(495)
; OTHER INFORMATION: n = a, c, t, or US-09-724-508-1
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; Batent No. 6294371
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6294371el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1045
; CURRENT APPLICATION NUMBER: US/09/621,233
; CURRENT FILING DATE: 200-07-21
; SOFTWARE: FastSRQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 897
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LOCATION: (472\(\times\)...(495)
OTHER INFORMATION: n = a, c, t, or g
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ORGANISM: Human
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APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 664072el motor proteins and methods for
TITLE OF INVENTION: No. 664072el motor proteins and methods for
TITLE OF INVENTION: Heir use
CURRENT FILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
PRIOR PLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
8.4%; Score 128.8; DB 4; Length 897;
Best Local Similarity 50.1%; Pred. No. 5.4e-27;
Matches 430; Conservative 0; Mismatches 356; Indels 72.
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LOCATION: (472)...(495)

// OTHER INFORMATION: n = a, c, t, or g

US-10-090-695-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 897
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Sequence 249, App Sequence 301, App Sequence 105, App Sequence 160, App Sequence 25129, App Sequence 25129, App Sequence 1485, App Sequence 31, Appli Sequence 3, Appli Sequence 31, Appli Sequence 313, App Sequence 318, App Sequence 318, App Sequence 288, App Sequence 288, App Sequence 288, App Sequence 288, App Sequence 288, App Sequence 268, App Sequence 268, App

23, Appl 57, Appl 1087, Ap

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

22135, A 2359, Ap 46568, A

34, Appl 34, Appl 27001, A

Sequence Sequence

Sequence 762, App Sequence 1053, Ap

9

Gaps

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0; Indels

DB 17; Length 1538;

Result

CGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC

OM nucleic

Run on:

Sequence:

Searched:

Database

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CGGCGATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAAGATTGGAGCTACTCGTCGTCCAC 120
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                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10797893
; Bedication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use
; FILE REPERBENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/99/724,224
; PRIOR APPLICATION NUMBER: US/99/724,224
; PRIOR PILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PSELSEQ for Windows Version 4.0
                                     US-09-883-096-1
US-10-287-226-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1538; I
Pred. No. 0;
; Mismatches
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Best Local Similarity 100.
Matches 1538; Conservative
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42092
42092
2517
33264
33264
33264
33264
33264
33267
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                       ; ORGANISM: Human
US-10-797-893-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1538
                                                                                                                                                                123.2
121.8
121.6
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107
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Sequence 288, Appli
Sequence 1, Appli
Sequence 131, Appli
Sequence 131, Appli
Sequence 1180, Ap
Sequence 1180, Ap
Sequence 11705, Ap
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Sequence 102, App
Sequence 7, Appli
                                                   November 10, 2004, 13:18:18; Search time 820.883 Seconds (without alignments) 10087.639 Million cell updates/sec
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                                                                                                     1 atgcagccgcggcggctcg.....accattgtcccacaatgtga 1538
                                                                                                                                                                                                                                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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6 US-10-334-143-102
US-10-797-893-7
1 US-09-225-300-288
7 US-10-797-893-5
1 US-09-803-5131
1 US-09-803-713-133
1 US-09-803-713-1393
3 US-10-087-122-1180
0 US-09-918-955-31705
3 US-10-087-122-1177
5 US-10-087-122-1177
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                              3611042 segs, 2692057975 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    - nucleic search, using sw model
                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                    US-10-797-893-3
1538
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2099
1464
2104
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Match 1
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98.8
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72.3
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Perfect score:
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1519
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1450.2
11112.4
1035.4
376.4
265
265
233.2
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8 6 8 6 8

	RESULT 2 US-10-334-143-102 is Sequence 102, Application US/10334143 is Publication No. US20040009549A1 is GENERAL INFORMATION: is APPLICANT: GRIGORIEL, IGON VACHESLAVOVICH is APPLICANT: SUDARSANAM, SUCHA itTLE OF INVENTION: MINASES IDENTIFIED WITH THE METHOD if TITLE OF INVENTION: MADER: US/10/334,143 icurrent APPLICATION NUMBER: US/10/334,143 icurrent APPLICATION NUMBER: 60/343,169 ip RIOR PILING DATE: 2001-12-31 inventer of the control	Ouery Match  98.8%; Score 1519; DB 16; Length 2099;  Best Local Similarity 99.9%; Pred. No. 0;  Matches 1530; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  Qy 6 GCCGCGGGCTCGACGCGACGACGACGACGACGACGACGACGACGCGGCG 65	Qy         66 ATCTCAGGAGCTGGTCGCTGTCGGCTAAGCAATTGGAGCTACTCGTCGTCGTCCACCTCCA         125	186 GATCCCCCTGTGTGGGGGCATGACCTGCTCTAGAGATTGCTAACTGGAGGAAC 196 GATCCCCCCTGTGTGCGGGCATGGACAGCTGCTCTTAGAGATTGCTAACTGGAGGAAC 209 GATCCCCCTGTGTGCGGGCATGGACAGCTGCTCTTGAGAGATTGCTAACTGGAGGAAC 246 CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGATACTGCAGCAG 1
CTCCAGCTCGCGTAAGGGTGGCTGTGCGGCCATTTGTGGATGGA	481 AGGAGGTGCCGAĞGCCGCATGGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCT 540	781 TGCCCCATTCGCCAGAGAGAAAACTCTACCTGATTGCTTGGTTGG		TCCTTATTGCCAACATTGCCCTGAGAGAGGCTTCTACCTAGACACAGTCTCCGCACTCAACCTTATTGCCAACATTGCCCAAGAGAGAG

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                                                                                                                    Sequence 7, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TILLE OF INVENTION: Christophe
; TITLE OF INVENTION: their use
; TILLE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797, 893
; CURRENT FILING DATE: 2004-03-09
; FRIOR PLICATION NUMBER: US/9/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARR: FRSESEQ for Windows Version 4.0
                                           95.0%; Score 1461; D
100.0%; Pred. No. 0;
ative 0; Mismatches
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Best Local Similarity 100.
Matches 1461; Conservative
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; TYPE: DNA
; ORGANISM: Human
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 288
LENGTH: 2104
                                                                                                                                                                                                     LOCATION: (44)
OTHER INPORMATION: n equals a,t,g, o
OTHER INPORMATION: n equals a,t,g, o
OTHER INPORMATION: n equals a,t,g, o
MANE/KEY: misc feature
LOCATION: (1323)
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
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; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA.01
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94.3%; Score 1450.2;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1457; Conservative 7; Mismatches U υ υ or ö or OTHER INFORMATION: n equals a,t,g, 671 ò g ò ö

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Matches 1113; Conservative
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; TYPE: DNA
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US-10-797-893-1
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Fublication No. US20040142397A1
GENERAL INFORMATION:
APULICANT: Beraud, Christophe
TITLE OF INVENTION: Novel motor proteins and met;
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1044
CURRENT APPLICATION NUMBER: US/10/797,893
CURRENT PILING DATE: 2004-03-09
FRIOR APPLICATION NUMBER: US/99/724,224
FRIOR APPLICATION NUMBER: 09/597,292
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-06-20
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GACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATC
                                                                                                               544 CTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTC
                                                                                                                                                      CTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCAGCGCTCCTCCCCGC
                                                                                                                                                                                                                                   AGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGCCCCCATTTCGCCAG
                                                                                                                                                                                                                                                                                                            798 CGAGAGGGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAACCGGCGCACAGGC
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US-00-56-23-131
US-00-56-23-131
Sequence 131 Application US/09960253
Fatent No. US20020123619A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT PAPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 491;
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; ORGANISM: Homo sapiens
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                                                                                         TCCTTATTGCCAACATTGCCCCTGAGACGCTTCTACCTAGACACACTCCA
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Publication No. US20040142397A1

GENERAL INFORMATION:

ITILE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

TITLE OF INVENTION: their use

CURRENT APPLICATION NUMBER: US/10/797,893

CURRENT APPLICATION NUMBER: US/09/724,224

PRIOR APPLICATION NUMBER: US/09/724,224

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR APPLICATION NUMBER: 09/597,292

PRIOR PILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                    1081 ACTITGCTGCCAGGTCCAAGGAGGTGATCAATCG 1114
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1036; Conserv
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US-10-797-893-5
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                                                                                                                               1207 CCCGAGGCCCTGAGGAAGAGGAGATTGGGAGCCCTGAGCCCATGGCAGCTCCAGCCTCTG
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 1180, Application US/10087192 |
| Publication No. US20020182586A1 |
| GENERAL INFORMATION: |
| APPLICANT: Morits, David W. |
| APPLICANT: Morits, David W. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: OAUCER |
| FILE REFERENCE: 529452000122 |
| CURRENT FILING DATE: 2002-03-01 |
| PRIOR APPLICATION NUMBER: US 09/747,377 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2000-12-03 |
| NUMBER OF SEC ID NOS: 2059 |
| SOFTWARE: FREESEQ for Windows Version 4.0 |
| LEASTH: 24525 |
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Mismatches
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CORGANISM: Homo sapiens
US-10-087-192-1180
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Matches 380;
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                                                                                                                                                                                                                                                                                              GGCAGCTCCAGCCTCTGCCTCCCAGAAACTCAGCCCCCTACAGAAGCTAAGCAGCATGGA 1309
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Pred. No. 1.1e-104;
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APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dramac, Radoje
APPLICANT: Dramac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Human Genes and Gene Products
FILE REFERENCE: 1624.002
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CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FASEUSEQ for Windows Version 4.0
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APPLICANT: Bacobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Rennedy, Giulia C.
APPLICANT: Kennedy, Giulia C.
APPLICANT: Kennedy, Giulia C.
APPLICANT: Lamson, George
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APPLICANT: Lamson, George
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Publication No. US20030044783A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-803-719-1937
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Best Local Similarity
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LENGTH: 386
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2939 AGGTATTAGACCTCTTGGATCCTGCATCAGGAGACCTCGTGATCCGCGAAGACTGCCGAG 2998
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                                                       260 CAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACATCTATGCAGG 319
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217 CGGTGCCTGAGGAGCTGGCATTAC-ATCTCGATGCTTGGCAGCCCAGAGCAACCTGGGGT
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OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(24291)
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Best Local Similarity
Matches 385; Conserv
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US-10-087-192-1177
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1493 CCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGAGGCCGCAGACAGGGGGCGAGGACCT 2552
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                                                               2553 GGGAAGCCCAGGAGCCTGAGCTAAGCACGAGACCTTTGTTCTTACCCCCAGGTGGACCAG
                                                                                                                                    2613 CGGGAACGTTTGGCCCCATTTCGCCAGCGAGAGGAAAACTCTACCTGATTGACTTGGCT
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: HYSEQ. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PRINCE DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FREESEQ for Windows Version 3.0
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; LOCATION: (1)....(464)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31705

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US-09-918-995-31705
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LENGTH: 464
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Sequence 24303, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Bavid R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANZEL DAVID R.
APPLICANT: HANZEL DAVID R.
APPLICANT: HANZEL SAVID R.
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APPLICANT: HANZEL SAVID R.
APPLICANT: HANZEL SAVID R.
APPLICANT: HANZEL SAVID R.
APPLICANT: APPLICATION NUMBER: US/10/29,386
CURRENT APPLICATION NUMBER: US/10/29,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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          938 TCAGGGCCTCCCTCGTGTACCTTATCGGGACAGCAGCTCACTCGCCTATTGCAGGAC 995
                                         214 TCAGGGCTCCCTCGTGTACCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGTC 271
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OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUE 5.00e-37
OTHER INFORMATION: BST HUMAN HIT: BE382882.1, EVALUE 1.00e-125
US-10-029-386-24303
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Pred. No. 5.4e-60;
0; Mismatches 1; Indels 0;
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Sequence 249, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20040005560A1e1

TITLE OF INVENTION: No. US20040005560A1e1

CURRENT APPLICATION WUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 249
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Best Local Similarity 99.6%;
Matches 231; Conservative C
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ORGANISM: Homo sapiens
FEATURE:
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US-10-108-260A-249
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LENGTH: 232
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OTITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10603
LENGTH: 531
3059 AGCACTTCCTTCCAGCCAGTAGAATCGAGCTGTAGGAGCCACCCGGCTTAACCAGGGCT 3118
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                                                                                                                             3119 CTTCCCGTAGTCACGCAGTGCTCTTGGTCAAGGTAAGGCCCGCTGACAGAAAGGCCTGGG 3178
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                                                                                                                                                                                                                                                                                 GAACGTTTGGCCCCATTTCGCCAGCGAGAAAACTCTACCTGATTGACTTGGCTGGG
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: WT HIT: AB0173341, EVALUE 0.000+00

OTHER INFORMATION: SWISSPROT HIT: Q14807, EVALUE 2.000-36

OTHER INFORMATION: BST_HUMAN HIT: BF975048.1, EVALUE 1.000-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10603, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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Matches 235; Conservative
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ORGANISM: Homo sapiens
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        DB 16; Length 2095;
Query Match 12.1%; Score 185.6; DB 16; Length Best Local Similarity 53.7%; Pred. No. 6.1e-46; Matches 464; Conservative 0; Mismatches 379; Indels
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SEQ ID NOS: 673
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Pred. No. 4.8e-37;
0; Mismatches 317; Indels 18;
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CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
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PRIOR PILING DATE: 2001-11-30
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PRIOR PILING DATE: 2001-04-39
PRIOR PILING DATE: 2002-02-04
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PRIOR PILING DATE: 2002-03-3
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Dipippo, Vincent A.,
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Spytek, Kimberley A.,
Taupier, Jr., Raymond
Vernet, Corine A.M.,
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Ji, Weizhen,
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Malyankar, Uriel M.,
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Miller, Charles E.,
Millet, Isabelle,
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Gangolli, Esha A.,
Gorman, Linda,
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Best Local Similarity 54.1%;
Matches 395; Conservative
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Shenoy, Suresh G.
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Ort, Tatiana,
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ORGANISM: Homo sapiens
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SEQ ID NO 301
LENGTH: 3374
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; Sequence 301, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:

US-10-287-226-301

APPLICANT: Agee, Michele L., APPLICANT: Alsobrook, John P., APPLICANT: Berghs, Constance,

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986 ATTGCAGGACTCTCTGGGTGGCTCAGCCCAGAGTACCTTATTGCCAACATTGCCCTGA 1045
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                                                                                    612 IGGGAAAACCTACACCATGCTGGGCACAGAGCCATGGCATCTATGTTCAGACCT 671
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Search completed: November 11, 2004, 01:20:38 Job time : 825.883 secs

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1st strand cDNA westrimmed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I. (bases I to 2057)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization
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                                               AL55550
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/plasmid="pCMVSPORT_6"
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llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 1919 JONE EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, doubble-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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CR590974.1 GI:50471781
HTC; CNSLT_cDNA.
HOMO sapiens (human)
HOMO sapiens (bordata; Craniata; Vertebrata; Euteleostomi; Mamanlia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1147 GCCTTGGGACCTGTTAAGCTGTCTCAGAAAGAATTGCTTGGTCCACCAGAGGCAAAGAA
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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98.4%; Score 1512.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1514; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1009YJ01"
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/tissue_type="Placenta
/plasmid="pCMVSPORT_6"
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Genoscope.

Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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2016 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI040YI06 of Placenta Cot 25-normalized of Homo sapiens (human).
CR590954.1 GI:50471761
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Libasa 1 to 2016)
Libas, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
 1261 CAGCCCCTACAGAAGCTAAGCATGCATGAACCCGGCCATGCTGGAGCCCTCCTCAGCTT
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="CSODI040Y106"
|/tissue_type="Placenta Cot/plasmid="pcMVSPORT_6"
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Encyclopedia Project of Genome Exploration Research Group in Riken Genome Encyclopedia Project of Genome Exploration Research Group In Riken Division of Experimental Animal Research in Riken contributed to
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                                          The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases I to 2055)
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
   n of a (2001)
 Functional annotation
Nature 409, 685-690 (2
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Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Togami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toga, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

L. Submitted (16-Apr.2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Xanagawa, 210-0045, Japan (E-mail:genome-resegnscriken.jp, VRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/note="kinesin superfamily protein KIF22"
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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URL.http://genome.gsc.riken.jp/
URL.http://fantom.gsc.riken.jp/
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/cell type="ES cells"
/clone_lib="RIKEN full
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (202)

E 6 (Dases I to 2056)

Adachi, J. Aizawa, K. Akahira, S., Akimura, T., Aono, H., Arai, A., Arawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirawa, T., Kato, H., Kawai, J., Kojino, Y., Konno, H., Kouda, M., Kowai, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Obno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
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           TCTGTTGAGTACCCCAAAGCGAGAGCGGATGGTGCTAATGAAGACAGTAGAAGAAGGA
                                                           cctactigaataccccaaagcgagaacgaatggtgcrcatgaagacagagagaaagaa
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1 (bases 1 to 1124)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31267547.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 ENRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mismo orprome" /mol type="mismo orprome" /mol type="mismo orprome" /mol type="mismo orprome" /mole="placentha" /mole="placentha" /mole="placentha" /mole="placentha" /mole="list strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized.
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EST 25-MAR-2004

OT 25-NORMALIZED Homo sapiens CDNA

AL545712

AL545712 Homo sapiens PLACENTA COT 25-NORM COLOR CSODI009YJ01 5-PRIME, mRNA sequence. AL545712.3 GI:45746191

DEFINITION ACCESSION VERSION

RESULT 6 AL545712 LOCUS

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                                                      /mol type="mcmology"
//mol type="mcmology"
//db xref="taxon:9606"
/clone="cSoD1041113"
/tissue type="placenth COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 1.8e-254;
3; Mismatches 0;
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     Location/Qualifiers
                                         organism="Homo
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                         AGAGGGAAAACTCTACCTGATTGACTTGGCTGGGKCAGAGGRCAACCGGSGCACAGGCAA
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                                                                                                                                                         GATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCT
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                                                        CCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGGGGAATATCCT
                                                                                                                                  GATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGCGGCACTTCCT
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BX337406 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODI041XII3 5-PRIME, mRNA sequence.
BX337406.2 GI:46274820
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI041AE07QP1&c=7766.r.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                            121 GCGTAAGGGTGGCTGTGCGACTGCGGCCATTTGTGGAACAGAACAGCGGGAGCAAGTGATC
                                                                                                                                                                     181 CCCCTGTGTGGGGGGGATGGACAGCTGCTCTAGAGATTGCTAACTGGAGGAACCACC
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                                             241 AGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAGGACA
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1. (Dases 1 to 1083)

2. Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

1. Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283903.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EWRY cedex - France

BP 191 91006 EWRY cedex - France

Bmail: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ScoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODGOO5CFO6QPl&c=7766.r.
Location/Qualifiers
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On May 5, 2003 this sequence version replaced gi:30368690.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library, was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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COT 25-NORMALIZED Homo sapiens
mRNA sequence.
                                           AGGTATTAGACCTCCTGGACCCTGCTTCGGGGGGACCTGGTAATCCGAGAAGACTGCCGGG
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          AGGTATTAGACCTCCTGGACCCTGCTTCGGGAGACCTGGTAATCCGAGAAGACTGCCGGG
                                                                                                                                      GGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTTGAGC
                                                                                                                                                                              541 GGAATATCCTGATTCCGGGTCTCTCCCAGAAGCCCATCAGTAGCTTTGCTGATTTTGAGC
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Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                 On May 2, 2003 this sequence version replaced gi:30337600.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSDORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 4.8e-248;
4; Mismatches 8;
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/db_xref="taxon:9606"
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Best Local Similarity 98.6%;
Matches 1003; Conservative
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/cell_line="HELA"
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/note="list strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                     942; DB 5; I
No. 2.4e-238;
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                                                                                               Similarity
                                                                                                         Matches 953;
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Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecox V sites of the pcMYSPORT & vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                              BX354166 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC015YH04 5-PRIME, mRNA sequence.
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/mol type="mRNA"
/db xref="taxon:9606"
/doine="CSOBCOLD5YH04"
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="Est strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 3.2e-236;
0; Mismatches 0; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Bukaryota; Metazoa; Chordata; Catarrhini; Hominid
1 (Dases 1 to 958)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:
                                                                                                                                                                                                                                            GI:46304510
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957 CCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCAC 1016
                                                                                                                                                                                                      Best Local Similarity
Matches 937; Conser
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1 (bases 1 to 1031)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                     GAGAAGCTATTAGACCTCCTGGCTTCGGGAGACCTGGTAATCCGAGAAGACTGC
                                                                     GAGCAACCTGGGGTGATCCCGCGGGCTCTCATGGACCTCCTGCAGCTCACAAGGGAGGAG
                                                                                                                                         GGTGCCGAGGGCCCATGGCCCTTTCTGTCACCATGTCTTACCTAGAGATCTACCAG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboration
CDNA Library Preparation: MGC Clone distribution information
Clone distribution: MGC clone distribution information can letun through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LLCM1948 row: 1 column: 06
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Location/Qualifiers
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/mol_type="mRNA"

/db_xref='taxon:9606"

/clone='InAces:5454101"

/tissue_type="astrocytoma grade IV, cell line"

/tlab_host="hulb (phage-resistant)"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC 98"

/note="Torgan brain; Vector: pOTB7; Site_1: Xho1; Site_2:

Rook1; cDNA made by oligo-dT priming. Directionally

cloned into EcoR1/Xho1 sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of

california, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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BX376199 1004 bp mRNA linear EST 27-APR-2004
BX376199 Homo sapiens NEUROBIASTOWA COT 25-NORWALIZED Homo sapiens
CDNA clone CSODC024YA10 5-PRIME, mRNA sequence.
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                      GATCCCCCCTGTGTGCGGGGGATGGACAGCTGCTCTCTAGAGATTGCTAACTGGAGGAAC
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                                                                                           CACCAGGAGACTCTCAAATACCAGTTTGATGCCTTCTATGGGGAGAGGAGTACTCAGCAG
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30452476. Contact: Genoscope - Centre National de Sequencage Genoscope - Genere National de Sequencage
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1 (bases 1 to 999)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

3 Full-length cDNA libraries and normalization

3 In pubblished (2001)

3 On Peb 15, 2001 this sequence version replaced gi:31283900.

3 Contact: Genoscope Gentre National de Sequencage

3 Genoscope - Centre National de Sequencage

3 Bp 191 91006 EVRY cedax - France

3 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

3 Est strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
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/call line="RAMOS CELL LINE"
/call line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/noce="Yector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) prImer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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CCTTATCGGGACAGCAAGCTCACTCGCCTATTGCAGGACTCTCTGGGTGGCTCAGCCCAC
                                                                       GCCGCGGGCGGCTCGACGCAGCAGACGCGACGCGAGATGCCGCAGCTTCAGCGGCGCG
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DG005CC06QP1&c=7766.r.
Location/Qualifiers
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                                                                                                                           CTCAACTTTGCTGCCAGG-TCCAAGGAGGTGATCAATCGGCCTTTT 1121
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96.8%; Pred. No. 7e-233;
ive 22; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG005YF11"
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/clone=trMcGE:5723623"
/lab_host="DH10B"
/lab_host="DH10B"
/clone=lib="NH10GC|125"
/clone=lorgan: Overy (pool of 3); Vector: pCMV-SPORT6;
/note="Organ: overy (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: Not1; RNA source pool of three overies, from females ranging in age from 38 to of three overies, from females ranging in age. from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA linear EST 20-FEB-2002 sapiens cDNA clone IMAGE:5723623
                                                                                                                                                                                                                                                    CGGGGGCACAGGCAACAAGGGSCTTCGGCTAAAAAGAGAGTGGAGCCATCAACACCTCCC 911
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Butheria; Primates; Catarrhini; Hominidae; Homo.

Cataria; Institutes of Health, Mammalian Gene Collection (MGC)

Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CONA Library Arrayed by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llhl.gov

Plate: LLAM12711 row: j column: 08

High quality sequence stop: 688.
                                                                                                                                                                CCCATTTCGCCAGCGAGAGAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAA 851
                                                                                                                                                                                                                                                                                                                     672 TGAGCGGCACTTCCTGCCAGCCAGTCGAAATCGGACTGTAGGAGCCACCCGGCTCAACCA 731
                                                                           732 GCGCTCCTCCCGCAGTCATGCTGGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTGGC
                                                                                                                                         CCCATTTCGCCAGCGAGAGAAAACTCTACCTGATTGACTTGGCTGGGTCAGAGGACAA
                                                                                                                                                                                                                              845 CCGGCGCACAGGCAACAAGGGCCTTCGGCT-AAAAGAGAGTGGAGCCATCAACACCTCCC
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                                                  GCGCTCCTCCCGCAGTCATGCTGTGCTCCTGGTCAAGGTGGACCAGCGGGAACGTTTGGC
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AGENCOURT_6491037 NIH_MGC_125 Homo
5', mRNA sequence.
BM546877 GI:18780186
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/db_xref="taxon:9606"
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Mol_type="mRNA"

Mol_type="taxon:9606"
/clone="CSODCO24YA10"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
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primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODC024BA05QP1&c=7766.r. Location/Qualifiers
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